

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 155.692 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071
Sequence: 1 EVQLVDSGDFVPGGSLRV.....IVEFLNRMTFCQSIITLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980a:.*
2: geneseqp1990a:.*
3: geneseqp2000a:.*
4: geneseqp2001a:.*
5: geneseqp2002a:.*
6: geneseqp2003a:.*
7: geneseqp2003bs:.*
8: geneseqp2004a:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4 AAB81987	Aab81987 Ganglioside
2	3026	98.5	582	4 AAB81991	Aab81991 Ganglioside
3	2780.5	90.5	583	4 AAB83156	Aab83156 Ganglioside
4	2760.5	89.9	581	4 AAB81972	Aab81972 Ganglioside
5	2750.5	89.6	579	6 AAE33444	AAE33444 KS antibo
6	2750.5	89.6	579	6 AAO30910	AAO30910 di-KS-ala
7	2719.5	88.6	575	8 ADPA2961	ADPA2961 Humanised
8	2621	85.3	580	6 AAO30915	AAO30915 di-NHS76
9	2589	84.3	580	6 AAO30913	AAO30913 di-NHS76
10	2240.5	73.0	447	6 AAE33522	AAE33522 Human AOC
11	2240.5	73.0	447	6 AAE33523	AAE33523 Human AOC
12	2238.5	72.9	449	6 AAO18400	AAO18400 Mature hu
13	2236.5	72.8	447	6 AAE33524	AAE33524 Human AOC
14	2236.5	72.8	450	8 ADH34587	ADH34587 023 heavy
15	2234.5	72.8	445	6 AAO31101	AAO31101 Human A2-
16	2233	72.7	449	6 AAB58273	AAB58273 Humanised
17	2233	72.7	468	6 ABP58275	ABP58275 Humanised
18	2232	72.7	451	8 ADH34584	ADH34584 008 heavy
19	2231.5	72.7	444	6 AAE33327	AAE33327 Humanised
20	2231.5	72.7	444	6 AAE34876	AAE34876 B1WA/8 a
21	2231.5	72.7	444	6 ADL15443	ADL15443 Humanised
22	2231.5	72.7	444	8 AD000851	AD000851 Humanised
23	2229.5	72.6	475	7 ADM47075	ADM47075 Mouse ant
24	2229	72.6	451	8 ADP88494	ADP88494 Humanised
25	2226	72.5	449	3 AAY68810	Aay68810 A rat hea

26	2222.5	72.4	477	4 AAU14288	AAU14288 Human nov
27	2221.5	72.3	446	7 ADP14425	ADP14425 208 anti-
28	2220	72.3	474	5 AAO14065	AAO14065 Heavy cha
29	2220	72.3	474	6 ABU08017	ABU08017 Human mon
30	2220	72.3	474	7 ADP65775	ADP65775 Human mon
31	2220	72.3	474	8 ADJ92515	ADJ92515 Human SOU
32	2219.5	72.3	461	6 ABR39847	ABR39847 Hu266 N56
33	2219.5	72.3	461	6 ABR39843	ABR39843 Hu266 N56
34	2219	72.3	451	6 ADH34586	ADH34586 021 heavy
35	2216.5	72.2	442	6 ABR39465	ABR39465 Humanised
36	2216.5	72.2	442	6 ABU08311	ABU08311 Humanised
37	2216.5	72.2	442	6 ABB80109	ABB80109 Heavy cha
38	2216.5	72.2	442	7 ADP94066	ADP94066 Humanised
39	2216.5	72.2	442	8 ADN61714	ADN61714 Humanised
40	2216.5	72.2	461	4 AAU07745	AAU07745 Humanised
41	2216.5	72.2	461	6 ABR39844	ABR39844 Hu266 N56
42	2216.5	72.2	461	6 ABR39848	ABR39848 Hu266 N56
43	2216	72.2	451	4 AAE12715	AAE12715 Human rec
44	2216	72.2	451	6 ABU58807	ABU58807 Mucin 1 (
45	2212	72.0	445	7 ADP14421	ADP14421 2811 anti

ALIGNMENTS

RESULT 1
AAB81987 standard; protein; 582 AA.
ID AAB81987;
AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KM Ganglioside; GD3; complementarily determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PE 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105086.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 41; Page 168-172; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
XX
Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.1e-153;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EVQLVESGGDGVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAAYISSGSGSTYY 60
    |||
    1 EVQLVESGGDGVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAAYISSGSGSTYY 60
Db
QY 61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
    |||
    61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
Db 61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
QY 121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
    |||
    121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
Db 121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
QY 181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
    |||
    181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
Db 181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
QY 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
    |||
    241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
Db 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
QY 301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
    |||
    301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
Db 301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
QY 361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
    |||
    361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
Db 361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
QY 421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
    |||
    421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
Db 421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
QY 481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
    |||
    481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
Db 481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
QY 541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582
    |||
    541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582
Db 541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582

RESULT 2
AAB8191
ID AAB8191 standard; protein; 582 AA.
XX
AC AAB8191;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SRQ ID NO: 57.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
OS Synthetic.
XX
PN MO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PA
XX PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX DR WPI; 2001-266143/27.
XX
XX PT New human type complementation-determining region-transplanted antibody
```

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PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
of e.g. tumors, with low antigenicity, little side effects but potent
activity in cancer.
XX
XX Claim 39; Page 175-179; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX Sequence 582 AA;
XX
Query Match 98.5%; Score 3026; DB 4; Length 582;
Best Local Similarity 98.3%; Pred. No. 4,9e-151;
Matches 572; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVQLVESGGDGVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAAYISSGSGSTYY 60
    |||
    1 EVQLVESGGDGVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAAYISSGSGSTYY 60
Db 1 EVQLVESGGDGVQPGGSLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVAAYISSGSGSTYY 60
QY 61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
    |||
    61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
Db 61 SDSVKGRTFISRDNSKNTLYIQMRSIARAEDSAVYFCTRYVKGATYYFDSWGQGTLLTVSSA 120
QY 121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
    |||
    121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
Db 121 STKGSPVFLAPASKSTSGGTALGCLVNDYFPEPTVSNMNSGALTSGVHTFPAVLQSSG 180
QY 181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
    |||
    181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
Db 181 LYSLSGVTVVPPSSSLGTQYIICNVNKKPSNTKVDKKEVPSCKDHTHCPCPAPELLGGP 240
QY 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
    |||
    241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
Db 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNS 300
QY 301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
    |||
    301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
Db 301 TYRVSIVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
QY 361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
    |||
    361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
Db 361 TKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
QY 421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
    |||
    421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
Db 421 QGNVFSCSVMEHALHNHYTQKSLSLSPGKAPTSSTTKTQQLQLEHLLDLQMLINGINNY 480
QY 481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
    |||
    481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
Db 481 KNPKLTIRMLTFRKYMFKKATLKHLCLEBEELKPIEEVYLNLAOSKNPFLRPDLISNINV 540
QY 541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582
    |||
    541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582
Db 541 IYVELKGSSETTFMCEYADETATIVFELNRMITFCQSIISTLT 582

RESULT 3
AAB83156
ID AAB83156 standard; protein; 583 AA.
XX
AC AAB83156;
XX
DT 02-JUL-2001 (first entry)
XX
DE Ganglioside GM2 antibody-related protein #1.
XX
KW Ganglioside; GM2; antibody; cytostatic; cancer.
XX
XX OS
XX PT unidentified.
```

PN WO200123431-A1.
 XX
 XX PD 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006775.
 XX
 XX 30-SEP-1999; 99JP-00278292.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Hanai N, Nakamura K, Niwa R;
 PI
 DR WPI; 2001-266142/27.
 XX
 PT Monoclonal antibodies against ganglioside GM2 combined with drugs,
 PT radioisotopes or proteins for treatment and diagnosis of cancer.
 XX
 PS Claim 43; Page 61-65; 80pp; Japanese.
 XX
 CC The present invention relates to derivatives of an antibody against
 CC ganglioside GM2. The antibody may be a monoclonal antibody or its
 CC fragments. The antibody is combined with a radioactive isotope, protein
 CC or small drug in the treatment and diagnosis of cancer
 XX
 SQ Sequence 583 AA;

Query Match 90.5%; Score 2780.5; DB 4; Length 583;
 Best Local Similarity 89.9%; Pred. No. 3.9e-118;
 Matches 526; Conservative 22; Mismatches 32; Indels 5; Gaps 2;

QY 1 EVOLVSGGDFVOPGSGSLRVSCAAGFAPSHYAMSWROAPGKLEMAVYISGSGSTY 60
 DB 1 EVOLVSGGAIVKVPKGVASVCKASGTYFTDYNMDWKSPGQGLEMMGIIYPPNNGSTGY 60

QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYKLGTY---PDSWGQGTLLTV 117
 DB 61 NQAFKSVITITVDITSTSTAMELHSLASEDTAVYYC--ATYGHYGYMFAVWGQGLTVTV 118

QY 118 SASTYKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 177
 DB 119 SASTYKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 178

QY 178 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPAPABEL 237
 DB 179 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPAPABEL 238

QY 238 GGPVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKRREQ 297
 DB 239 GGPVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKRREQ 298

QY 298 YNSTYRVSVLTVLHODMNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYTLPPSR 357
 DB 299 YNSTYRVSVLTVLHODMNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYTLPPSR 358

QY 358 DELTKQVSLTCLVKGFPYSDIAVEWESNGOPENNYKTPPVLDSDGSFELYSLKLTVDKS 417
 DB 359 DELTKQVSLTCLVKGFPYSDIAVEWESNGOPENNYKTPPVLDSDGSFELYSLKLTVDKS 418

QY 418 RMOQGVFSCSVNHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLINGI 477
 DB 419 RMOQGVFSCSVNHEALHNHYTQKSLSLSPGKAPTSSSTKKTQLQLEHLLDLQMLINGI 478

QY 478 NNYKPKLTMLTFKFPMPKKAATLKLQCLEBEELKLEEVNLIAQSKNFHLPRDLISN 537
 DB 479 NNYKPKLTMLTFKFPMPKKAATLKLQCLEBEELKLEEVNLIAQSKNFHLPRDLISN 538

QY 538 INIVTLELKGSETTPECEVADETATVEFLNRWTTTPOSITSTLT 582
 DB 539 INIVTLELKGSETTPECEVADETATVEFLNRWTTTPOSITSTLT 583

ID AAB81972 standard; protein; 581 AA.
 XX
 XX AAB81972;
 AC
 XX 03-JUL-2001 (first entry)
 DT
 XX Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
 DE
 XX Ganglioside, GD2; complementation determining region; CDR; antibody;
 KW mouse; cancer.
 KM
 XX Synthetic.
 OS
 PN WO200123573-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-JP006773.
 XX
 PR 30-SEP-1999; 99JP-00278290.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 PI
 DR WPI; 2001-266163/27.
 XX
 PT Human type complementation-determining domain transplanted antibody and
 PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
 PT e.g. tumors, has low antigenicity, little side effects but potent
 PT activity in cancer.
 XX
 PS Example 3; Page 111-114, 123pp; Japanese.
 XX
 CC The present invention describes an antibody, which can react specifically
 CC with ganglioside GD2, and is transplanted with a human type
 CC complementation-determining domain (CDR), or its fragments. The antibody
 CC and its derivatives are useful in diagnosis and therapy of tumors,
 CC particularly cancer diagnosis. The present sequence is a protein used in
 CC the exemplification of the invention
 XX
 SQ Sequence 581 AA;

Query Match 89.9%; Score 2760.5; DB 4; Length 581;
 Best Local Similarity 90.0%; Pred. No. 4.3e-137;
 Matches 524; Conservative 22; Mismatches 35; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVOPGSGSLRVSCAAGFAPSHYAMSWROAPGKLEMAVYISGSGSTY 60
 DB 1 QVOLQSGGGLVAPSGQTLSTITCTVSGFSLASVNIHVRQPPGKLEMLGVYNAQGS-TNY 59

QY 61 SDSVKGFTISRDNKNTLYLQMRSLRAEDSAVYFCTRYKLGTYFDSWGQGTLLTVSSA 120
 DB 60 NSALMGRILTIKSNQVFLKMSLTAAADTAVYYCAKSDVSWFAVWGQGLTVVSSA 119

QY 121 STGSPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSSG 180
 DB 120 STGSPVFPPLAPSSKSTSGGTALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSSG 179

QY 181 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPAPABELLGP 240
 DB 180 LYSLSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDTHTCPPAPABELLGP 239

QY 241 SVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKRREQYNS 300
 DB 240 SVFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKRREQYNS 299

QY 301 TYRVSVLTVLHODMNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYTLPPSRDEL 360
 DB 300 TYRVSVLTVLHODMNGKEYKCKVSNKALPAPIEKTISRKAGQPREPQVYTLPPSRDEL 359

QY 361 TKQVSLTCLVKGFPYSDIAVEWESNGOPENNYKTPPVLDSDGSFELYSLKLTVDGSRMQ 420

```
Db      360  TRKNQVSLTCLVKGFPSPDIAVEMESNGPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419
QY      421  OGNVFCSCVMHEALHNHYTQKSLSPGKAPTSSTTKTQLOLEHLLDLQMLINGINN 480
Db      420  OGNVFCSCVMHEALHNHYTQKSLSPGKAPTSSTTKTQLOLEHLLDLQMLINGINN 479
QY      481  KNPKLTRMLTFKFPMPKKATELKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 540
Db      480  KNPKLTRMLTFKFPMPKKATELKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 539
QY      541  IVLELKGETTFMCEYADETATIVFPLNRWITFCQSIISTLT 582
Db      540  IVLELKGETTFMCEYADETATIVFPLNRWITFCQSIISTLT 581

RESULT 5
AAE33444
ID      AAE33444 standard; protein, 579 AA.
XX
AC      AAE33444;
XX
DT      02-APR-2003 (first entry)
XX
DE      KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.
XX
KW      Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpcAM;
KM      cancer; gene therapy; interleukin-2; IL2; fusion protein.
XX
OS      Unidentified.
XX
PN      WO200290566-A2.
XX
PD      14-NOV-2002.
XX
PF      03-MAY-2002; 2002WO-US013844.
XX
PR      03-MAY-2001; 2001US-0288564P.
XX
PA      (LEXI-) LEXIGEN PHARM CORP.
XX
PI      Gillies SD, Lo K, Qian X;
XX
DR      WPI; 2003-111985/10.
XX
DR      N-PSDB; AAD51139.
XX
PT      New recombinant anti-EPCAM antibody having an amino acid sequence
PT      defining an immunoglobulin light or heavy chain framework region, useful
PT      for the diagnosis, prognosis and treatment of cancer.
XX
PS      Disclosure; Page 80-82; 82pp; English.
XX
CC      The present invention relates to novel recombinant anti-EPCAM (human
CC      epithelial cell adhesion molecule) antibodies comprising an amino acid
CC      sequence defining an immunoglobulin light or heavy chain framework
CC      region. Sequences of the present invention are useful for the diagnosis,
CC      prognosis and treatment of cancer. They are also used in gene therapy.
CC      The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)
CC      fusion protein. This sequence is used to illustrate the method of the
CC      invention
XX
SQ      Sequence 579 AA;

Query Match      89.6%; Score 2750.5; DB 6; Length 579;
Best Local Similarity 88.5%; Pred. No. 1.4e-136;
Matches 516; Conservative 32; Mismatches 30; Indels 5; Gaps 2;
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```
QY      120  ASTKGSVPPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db      117  ASTKGSVPPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
QY      180  GLYSLSSVTVBSSSLGTQTYICNVNHPKSNTRVDKVPKSCDTHTCPPCAPPELLGG 239
Db      177  GLYSLSSVTVBSSSLGTQTYICNVNHPKSNTRVDKVPKSCDTHTCPPCAPPELLGG 236
QY      240  PSVFLPPPKPKDTLMISRPPEVTCVVDVSHEDPVRKFMWYDGVENHAKTKPRBEQYN 299
Db      237  PSVFLPPPKPKDTLMISRPPEVTCVVDVSHEDPVRKFMWYDGVENHAKTKPRBEQYN 296
QY      300  STYRVSVLTVALHODPLNGEKYCKVKSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDE 359
Db      297  STYRVSVLTVALHODPLNGEKYCKVKSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDE 356
QY      360  LTRKNQVSLTCLVKGFPSPDIAVEMESNGPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 419
Db      357  LTRKNQVSLTCLVKGFPSPDIAVEMESNGPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 416
QY      420  OGNVFCSCVMHEALHNHYTQKSLSPGKAPTSSTTKTQLOLEHLLDLQMLINGINN 479
Db      417  OGNVFCSCVMHEALHNHYTQKSLSPGKAPTSSTTKTQLOLEHLLDLQMLINGINN 476
QY      480  YKNPKLTRMLTFKFPMPKKATELKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 539
Db      477  YKNPKLTRMLTFKFPMPKKATELKHLCLEBELKPLEEVLNLAQSKNPHLRPRDLISNIN 536
QY      540  IVLELKGETTFMCEYADETATIVFPLNRWITFCQSIISTLT 582
Db      537  IVLELKGETTFMCEYADETATIVFPLNRWITFCQSIISTLT 579

RESULT 6
AAO30910
ID      AAO30910 standard; protein, 579 AA.
XX
AC      AAO30910;
XX
DT      22-SEP-2003 (first entry)
XX
DE      di-KS-ala-IL2 (D20T) variant protein.
XX
KW      Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KM      gene therapy; immunoglobulin; Ig; fusion protein; human.
XX
OS      Homo sapiens.
OS      Unidentified.
OS      Chimeric.
XX
PN      WO2003048334-A2.
XX
PD      12-JUN-2003.
XX
PF      04-DEC-2002; 2002WO-US038780.
XX
PR      04-DEC-2001; 2001US-0337113P.
PR      12-APR-2002; 2002US-0371966P.
XX
PA      (EMDL-) EMD LEXIGEN RES CENT CORP.
XX
PI      Gillies SD;
XX
DR      WPI; 2003-S13757/48.
XX
PT      New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT      moiety, useful for preparing a composition for treating cancer, viral
PT      infections or immune disorders.
XX
PS      Example 10; Page 60-63; 71pp; English.
XX
CC      The invention relates to cytokine fusion proteins with increased
```


Query Match	Similarity	84.3%	Score 2589	DB 6	Length 580
Beet	Local	85.1%	Pred. No. 4, 4e-128,		
Matches	497	Conservative	29	Mismatches	52
				Indels	6
				Gaps	5
QY	1	EVQLVESGGD	DFQPGSGLRVSCAAGFAFSH-YAMSWYQAPGKGLIEWVAISSGGSGTY	59	
DB	1	QVQLDQESG	BGLVKPSETLSLTCAVSGYSSISGTYGMIRQPKGLEIMGISYHSGS-TY	59	
QY	60	YSDSVKGRFTIS	RDNSSKNTLYIQMSLRRAEDSAVYFCTRVKLGITYYFDSWGGTLLTVSS	119	
DB	60	YNPSTLSKRTTIS	VDPSRKQPSFKLSLSPADAPAVYYCARGKWSK--FDWGGTLLTVSS	117	
QY	120	-ASTGSPVFLA	PSKSTSGTALGCLVQYFPEPTVSNSSGALTSGYHTFAVYQS	178	
DB	118	GAISTGPSFPLA	PCSRSTSESTALGCLVQYFPEPTVSNSSGALTSGYHTFAVYQS	177	
QY	179	SGLYSLSSVTV	PPSSSLGTQYICVNNHKPSNTKYDKKVEPKSCDKHTCCPCAPPELLG	238	
DB	178	SGLYSLSSVTV	PPSSNFGQTGYTCVNDHKPSNTKYDKVEPKSCDKHTCCPCAP--VA	236	
QY	239	GPSVFLPPEPK	KDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVYHNAKTKRREQY	298	
DB	237	GPSVFLPPEPK	KDTLMISRTPEVTCVVVDVSHEDPEVQFNNYVDSGEVYHNAKTKRREQA	296	
QY	259	NSTYVSVSLT	LYLHDDMTNGEKYKCKVSKYKLPALIEKTIISKAKQPREPVYTLPERSD	358	
DB	257	OSTFVSVSLT	LYVHDDMTNGEKYKCKVSKYKLPALIEKTIISKAKQPREPVYTLPERE	356	
QY	359	ELTKNQVSLT	CLVKGFPYSPDIAVEWESNGQPENNKFTTPPVLDSDGSFFLYSKLTVDYDSR	418	
DB	357	ELTKNQVSLT	CLVKGFPYSPDIAVEWESNGQPENNKFTTPPMLDSGSEFLYSKLTVDYDSR	416	
QY	419	WQGGVFGCS	VNHEALAHNYTKSISLSPKATPSSSTFKTQLQLEHLILDLOMTLNGIN	478	
DB	417	WQGGVFGCS	VNHEALAHNYTKSATAFPAGAPTSSTFKTQLQLEHLILDLOMTLNGIN	476	
QY	479	NYKNKRLRML	TFKKYMPKKAETELNHLCLDEELKPLEEYVNLAAQSKPHLRPRLISNI	538	
DB	477	NYKNKRLRML	TFKKYMPKKAETELNHLCLDEELKPLEEYVNLAAQSKPHLRPRLISNI	536	
QY	539	NYIVLELKG	SETTFMCEYADETATIVPEFLNRWITFCQSIISITLT	582	
DB	537	NYIVLELKG	SETTFMCEYADETATIVPEFLNRWITFCQSIISITLT	580	
RESULT 10					
ID	AAE33522	standard; protein; 447 AA.			
XX	AAE33522;				
XX	DT	02-APR-2003 (first entry)			
XX	DE	Human AQC2 heavy chain protein.			
XX	XX	Human, very late activation antigen; VLA-1; beta1 containing integrin; immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendinitis; bursitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type 1 diabetes; myaethenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polyomyelitis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia.			
OS	Homo sapiens.				
XX	XX	WO200283854-A2.			

[illegible]

QY 361 TKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTPPVLDSGDFLYSKLTVDKSRMQ 420
 DB 360 TKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTPPVLDSGDFLYSKLTVDKSRMQ 419
 QY 421 QGNVFCSCVMHEALNHHTYOKSLSPG 448
 DB 420 QGNVFCSCVMHEALNHHTYOKSLSPG 447

RESULT 11

AAE33523

ID AAE33523 standard; protein; 447 AA.

AAE33523;

DT 02-APR-2003 (first entry)

DE Human AOC2 heavy chain mutant protein, hAAOC2.

KM Human; very late activation antigen; VLA-1; beta1 containing integrin;
 KM immunological disorder; inflammatory disorder; skin related condition;
 KM psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KM fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KM fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KM irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KM atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;
 KM gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KM osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KM systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KM renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polyneuritis;
 KM hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KM graft versus host disease; myocardial ischaemia; mutant; mutein.

OS Homo sapiens.

PN WO200283854-A2.

PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011521.

PR 13-APR-2001; 2001US-0283794P.

PR 06-JUL-2001; 2001US-0303689P.

XX (BIOJ) BIOGEN INC.

PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;

DR WPI; 2003-093009/08.

PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.

PS Example 23; Page 91-92; 248pp; English.

CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; beta1 containing integrin) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headache, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,

CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human AOC2 heavy chain mutant protein, hAAOC2
 SQ Sequence 447 AA;

Query Match 73.0%; Score 2240.5; DB 6; Length 447;
 Best Local Similarity 94.9%; Pred. No. 6.8e-110;
 Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVQLVESGGDGVFQPGSLRVSCAASGFAFSHYAMSWVQAQAPGKLEWVAIYISGGSGITY 60
 DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTFSRYSWVQAQAPGKLEWVAIYISGGH-FYY 59
 QY 61 SDYVKGRFTISRDNKNTLYLQMSLRADSAVYFCTRYKLTGYTFDSKGGSTLTIVSSA 120
 DB 60 LDSVKGRTISRDNKNTLYLQMSLRADPAVYCTRGFDGQYFDWGQSTLTIVSSA 119
 QY 121 STKGSPVPLAPSSKSTGGTAAGCLVXDYFPEPVTVSMNSGALTSGVHFPVAVLQSSG 180
 DB 120 STKGSPVPLAPSSKSTGGTAAGCLVXDYFPEPVTVSMNSGALTSGVHFPVAVLQSSG 179
 QY 181 LYSLSVVTVVSSSISGTQTYICNVNKKPSNTEKVDKVPKSCDKHTHCPCPAPRLGGP 240
 DB 180 LYSLSVVTVVSSSISGTQTYICNVNKKPSNTEKVDKVPKSCDKHTHCPCPAPRLGGP 239
 QY 241 SVFLFPPPKDTLMISRPETCTCVVDYSHEDPEVKFMYVDGVVHNAKTPREEQINS 300
 DB 240 SVFLFPPPKDTLMISRPETCTCVVDYSHEDPEVKFMYVDGVVHNAKTPREEQINS 299
 QY 301 TYRIVSVTLVHODPLNGEKYCKVSNKALPAPIKRTISKAKGPREPOVTLPPSRDEL 360
 DB 300 TYRIVSVTLVHODPLNGEKYCKVSNKALPAPIKRTISKAKGPREPOVTLPPSRDEL 359
 QY 361 TKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTPPVLDSGDFLYSKLTVDKSRMQ 420
 DB 360 TKQVSLTCLVKGFPSPDIIVEMESNGQPENNYKTPPVLDSGDFLYSKLTVDKSRMQ 419
 QY 421 QGNVFCSCVMHEALNHHTYOKSLSPG 448
 DB 420 QGNVFCSCVMHEALNHHTYOKSLSPG 447

RESULT 12

AAO18400

ID AAO18400 standard; protein; 449 AA.

AAO18400;

DT 11-OCT-2002 (first entry)

DE Mature humanised murine CBE11 heavy chain variable domain.

KM Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;

KM neoplasia; LT-beta-R; light chain; heavy chain; variable region.

OS Mus sp.

OS Synthetic.

PN WO200230986-A2.

PD 18-APR-2002.

PF 12-OCT-2001; 2001WO-US0322140.

PR 13-OCT-2000; 2000US-0240285P.

PR 13-MAR-2001; 2001US-0275289P.

PR 21-JUN-2001; 2001US-029987P.

XX (BIOJ) BIOGEN INC.

PI Garber E, Lyne P, Saldanha JW;
 XX
 DR WPI; 2002-583337/62.
 XX
 PT New humanized anti-lymphotoxin-beta receptor antibody, useful for
 PT treating or reducing the advancement, severity or effects of neoplasia,
 PT particularly solid tumors (i.e. carcinomas) including colorectal cancer
 PT and breast cancer.
 XX
 XX Example 5, Page 25-26; 41pp; English.
 XX
 CC The present invention relates to humanised anti-lymphotoxin beta receptor
 CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
 CC binding antibody CBE11 and can be used to treat neoplasia in humans. The
 CC present sequence is a humanised murine CBE11 heavy chain variable region
 XX
 XX Sequence 449 AA;
 SQ
 Query Match 72.9%; Score 2238.5; DB 5; Length 449;
 Best Local Similarity 94.0%; Pred. No. 8.7e-110;
 Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;
 QY 1 EVOLVESGDFVPGSLRVSCAAGFAFSHYAMSWROAPGKLEWVAIISGSGSTYY 60
 DB 1 EVOLVESGGGLVVKGSLRLSCAASGFTFSYVYWRQAPEGKLEWVAITISDGSSTYY 60
 QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRYKLGTYRDSMGQGLTLTVSS 119
 DB 61 PDSVKGKFTISRDNKNTLYLQNRSLRAEDTAAYVYCARENGKNTFYFDYMGQGLTLTVSS 120
 QY 120 ASTKGPEVFPPLAPSSKSTSGGTALGCLVNDYPEPPTVSNAGALNSGVHTPPAVYVQSS 179
 DB 121 ASTKGPEVFPPLAPSSKSTSGGTALGCLVNDYPEPPTVSNAGALNSGVHTPPAVYVQSS 180
 QY 180 GLVSLSSVTVVPSSSLGCTGYIICNVNKKPSNTKVDKVEPKSCDKHTCPCPAPELLGSP 239
 DB 181 GLVSLSSVTVVPSSSLGCTGYIICNVNKKPSNTKVDKVEPKSCDKHTCPCPAPELLGSP 240
 QY 240 PSYFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKPREQYN 299
 DB 241 PSYFLPFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKPREQYN 300
 QY 300 STRRVSVTLVTLHODMNGKVEYKCKVKNKALPAIEKTIKAKQGPPEPVYTLPPSRDE 359
 DB 301 STRRVSVTLVTLHODMNGKVEYKCKVKNKALPAIEKTIKAKQGPPEPVYTLPPSRDE 360
 QY 360 LTRKNQVSLTCLVKGFPSPDIAVEWESNGOPENNYKTPVLDSDGSFELYSKLTVDSRW 419
 DB 361 LTRKNQVSLTCLVKGFPSPDIAVEWESNGOPENNYKTPVLDSDGSFELYSKLTVDSRW 420
 QY 420 QCGNVFSCSYMHKALNNHYTOKSLISLSPG 448
 DB 421 QCGNVFSCSYMHKALNNHYTOKSLISLSPG 449
 RESULT 13
 AAE33524 standard; protein; 447 AA.
 ID AAE33524
 XX
 AC AAE33524;
 XX
 DT 02-APR-2003 (first entry)
 XX
 XX Human AOC2 heavy chain mutant protein, hsaAOC2.
 XX
 KM Human; very late activation antigen; VLA-1; beta1 containing integrin;
 KM immunological disorder; inflammatory disorder; skin related condition;
 KM psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KM fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KM fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KM irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KM atherosclerosis; thyroiditis; aplastic anaemia; periarthritis nodosa;
 KM gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;

KM osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KM systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KM renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KM hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KM graft versus host disease; myocardial ischaemia; mutant; mutein.
 OS Homo sapiens.
 XX
 XX W0200283854-A2.
 XX
 XX 24-OCT-2002.
 PD
 PF 12-APR-2002; 2002W0-US011521.
 XX
 XX 13-APR-2001; 2001US-0283794P.
 PR 06-JUL-2001; 2001US-0303689P.
 XX
 XX (BIOV) BIOGEN INC.
 PA
 PI Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 XX
 XX WPI; 2003-093009/08.
 DR
 XX
 XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.
 XX
 XX Example 23; Page 92; 248pp; English.
 XX
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; beta1 containing integrin) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarthritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity) or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human AOC2 heavy chain mutant protein, hsaAOC2
 XX
 XX Sequence 447 AA;
 SQ
 Query Match 72.8%; Score 2236.5; DB 6; Length 447;
 Best Local Similarity 94.6%; Pred. No. 1.1e-109;
 Matches 424; Conservative 4; Mismatches 19; Indels 1; Gaps 1;
 QY 1 EVOLVESGDFVPGSLRVSCAAGFAFSHYAMSWROAPGKLEWVAIISGSGSTYY 60
 DB 1 EVOLVESGGGLVVKGSLRLSCAASGFTFSYVYWRQAPEGKLEWVAITISDGSSTYY 59
 QY 61 SDVKGKFTISRDNKNTLYLQNRSLRAEDSAVYFCTRYKLGTYRDSMGQGLTLTVSSA 120
 DB 60 LPSVKGKFTISRDNKNTLYLQNRSLRAEDTAAYVYCARENGKNTFYFDYMGQGLTLTVSSA 119
 QY 121 STKGPEVFPPLAPSSKSTSGGTALGCLVNDYPEPPTVSNAGALNSGVHTPPAVYVQSSG 180
 DB 120 STKGPEVFPPLAPSSKSTSGGTALGCLVNDYPEPPTVSNAGALNSGVHTPPAVYVQSSG 179
 QY 181 LVSLSVTVVPSSSLGCTGYIICNVNKKPSNTKVDKVEPKSCDKHTCPCPAPELLGSP 240
 DB 180 LVSLSVTVVPSSSLGCTGYIICNVNKKPSNTKVDKVEPKSCDKHTCPCPAPELLGSP 239

QY 241 SVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPEQYN 300
 CC binding molecules is useful for preventing and treating neoplastic
 CC disorder or disease such as leukemias, neoplasms, bile duct carcinoma,
 CC bladder carcinoma, viral disorder or disease associated with severe acute
 CC respiratory syndrome (SARS), herpes simplex virus (HSV), hepatitis B
 CC virus (HBV), HIV and bacterial disorder or disease associated with
 CC Mycobacterium tuberculosis, Pseudomonas aeruginosa and Vibrio cholerae.
 Db 240 SVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPEQYN 299
 QY 301 TYRIVSVLTGLVHQMVLNGEKYKCKVSNKALPAPIEKTISAKAQPREPOVYTLPPSRDEL 360
 SQ Sequence 450 AA;
 Db 300 TYRIVSVLTGLVHQMVLNGEKYKCKVSNKALPAPIEKTISAKAQPREPOVYTLPPSRDEL 359
 QY 361 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPLVDSGSPFLYSKLTVDKSRMQ 420
 Query Match 72.8%; Score 2236.5; DB 8; Length 450;
 Best Local Similarity 93.1%; Pred. No. 11e-109; Indels 3; Gaps 2;
 Matches 420; Conservative 12; Mismatches 16; Indels 3; Gaps 2;
 Db 360 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPLVDSGSPFLYSKLTVDKSRMQ 419
 QY 421 QGNVFSCSVNHEALHNHYTQKSLSLSPG 448
 RESULT 14
 ADH34587
 ID ADH34587 standard; protein; 450 AA.
 AC ADH34587;
 DT 11-MAR-2004 (first entry)
 DE 023 heavy chain.
 KM antibody; OX40 receptor; specific phage antibody; bcfv, CD134, ACT-4;
 KM ACT33; TNF receptor family; CD4+; T cell; tumour necrosis factor;
 KM proliferation; immune response; memory cell; tumour; bacterial; viral;
 KM antigen; leukaemia; neoplasm; bile duct carcinoma; bladder carcinoma;
 KM severe acute respiratory syndrome; SARS; herpes simplex virus; HSV;
 KM hepatitis B virus; HBV; HIV; Mycobacterium tuberculosis;
 KM Pseudomonas aeruginosa; Vibrio cholerae.
 OS Synthetic.
 PN WO2003106498-A2.
 XX 24-DEC-2003.
 PF 13-JUN-2003; 2003WO-BE006341.
 PR 13-JUN-2002; 2002WO-NL000389.
 PA (CRUC-) CRUCELL HOLLAND BV.
 PI Bakker ABH, Meester-Rood PML, Bakker AQ;
 DR WPI; 2004-082162/08.
 DR N-PSDB; ADH34601.
 PT Novel agonistic binding molecule capable of binding to and stimulating
 human OX-40-receptor, useful for modulating T-cell proliferation.
 XX Claim 4; SEQ ID NO 28; 148bp; English.
 CC This sequence represents the heavy chain of a selected phage antibody
 CC against human OX40 receptor. OX40 receptor, (also known as CD134, ACT-4,
 CC ACT33) is a member of the TNF receptor family which is expressed on
 CC activated CD4+ T cells. Triggering of this receptor enhances the
 CC proliferation of CD4+ T-cells during an immune response and influences
 CC the formation of CD4+ memory cells. A human OX40 receptor specific phage
 CC antibody (scfv) represents the agonistic binding molecule of the
 CC invention which is capable of binding to and stimulating the human OX-40-
 CC receptor. The binding molecules of the invention are useful as a
 CC medicament for treating neoplastic, viral or bacterial disorder or
 CC disease, for stimulating T-cells in vitro and for enhancing the immune
 CC response in a human or animal against a tumour, bacterial or viral
 CC antigen. They are useful for modulating T-cell response in a human which
 CC involves administration to the human, where the modulation includes
 CC stimulation of T-cells. A pharmaceutical composition containing the

CC binding molecules is useful for preventing and treating neoplastic
 CC disorder or disease such as leukemias, neoplasms, bile duct carcinoma,
 CC bladder carcinoma, viral disorder or disease associated with severe acute
 CC respiratory syndrome (SARS), herpes simplex virus (HSV), hepatitis B
 CC virus (HBV), HIV and bacterial disorder or disease associated with
 CC Mycobacterium tuberculosis, Pseudomonas aeruginosa and Vibrio cholerae.
 Db 419 WOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 450
 QY 1 EVQLVESGGDFVQPGSRLVSGCAASGFAPSHYAMGVRQAPEKGLIEWAYISSGSGITY 60
 Db 1 EVQLVESGGGVLVHPGSGRLSCASGFTFPSSAHMHWQAPOKGLIEWASLITGG-GRYY 59
 QY 61 SDSVKGRFTISRDNSKNTLYIQLMRSLRADDSAVYFCTRYK--LGITYRDSWGQGTLLTVS 118
 Db 60 ADSVWGKRFITSRDNSKNTLYIQLMNSLRADDTAVYVCARDYDVMGLYFEDYMQGTLLTVS 119
 QY 119 SASTGSPSVPLAPSSKTSGGTALGCLVNDYPEPEPTVSNAGSLTSGVHTPPAVIQS 178
 Db 120 SASTGSPSVPLAPSSKTSGGTALGCLVNDYPEPEPTVSNAGSLTSGVHTPPAVIQS 179
 QY 179 SGLYSLSSVAVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELIG 238
 Db 180 SGLYSLSSVAVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKHTCPCPAPELIG 239
 QY 239 GPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPEQY 298
 Db 240 GPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPEQY 299
 QY 299 NSTYRVSVLTGLVHQMVLNGEKYKCKVSNKALPAPIEKTISAKAQPREPOVYTLPPSRD 358
 Db 300 NSTYRVSVLTGLVHQMVLNGEKYKCKVSNKALPAPIEKTISAKAQPREPOVYTLPPSRD 359
 QY 359 ELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPLVDSGSPFLYSKLTVDKSR 418
 Db 360 EMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPLVDSGSPFLYSKLTVDKSR 419
 QY 419 WOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 449
 Db 420 WOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 450
 RESULT 15
 AAO31101
 ID AAO31101 standard; protein; 445 AA.
 AC AAO31101;
 DT 06-OCT-2003 (first entry)
 DE Human A2-G8 SCF antibody heavy chain variable and constant region.
 KM Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
 KM steel factor; c-kit ligand; gene therapy.
 OS Homo sapiens.
 PN WO2003051311-A2.
 XX 26-JUN-2003.
 PF 16-DEC-2002; 2002WO-US040227.
 PR 17-DEC-2001; 2001US-0342174P.
 PA (FARB) BAYER CORP.
 PI Takeuchi T, Tomkinson A, Neben S;

DR WPI; 2003-523500/49.

XX
PT New purified human antibody that binds to stem cell factor protein,
PT useful for preparing a composition for treating asthma.XX
PS Claim 9; Page 47; 94pp; English.XX
CC The invention provides human antibodies that bind to stem cell factor
CC (SCF) protein. SCF is also known as mast cell growth factor, steel factor
CC or c-kit ligand. Antibodies of the invention are useful for preparing
CC compositions for treating asthma. They are also used in gene therapy. The
CC present sequence is human SCF antibody heavy chain variable and constant
CC regionXX
SQ Sequence 445 AA;

Query Match 72.8%; Score 2234.5; DB 6; Length 445;

Best Local Similarity 94.4%; Pred. No. 1,4e-109;

Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

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QY 4 LVSSGDFVPGGSLRVSCAASGFAFSHYAMSTROAPGKLEWVAIYSSGGSGTYSDS 63
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 LVSSGGGLVPGGSLRLSCAASGFTFSSYAMSWVROAPGKLEWVAISGGSGSTYYADS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 VKGRFTISRDNKNTLYLQMRSLRAEDSAVYFCTRVNLGTYYPDSWGQTLTLTVSSASTK 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VKGRFTISRDNKNTLYLQMRSLRAEDTAAYTCARDFPA-HFDVMGQGLTVTVSSASTK 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 124 GPSVFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSGLYS 183
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 120 GPSVFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSGLYS 179
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 184 LSSGVTVYPSSSLGTQYIYICVNNHKSNTKYDKKVEPKSCDKHTCPCPAPPELLGSPVF 243
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 180 LSSGVTVYPSSSLGTQYIYICVNNHKSNTKYDKKVEPKSCDKHTCPCPAPPELLGSPVF 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 244 LFPKPKPDLMISRTPEVTCVVDVSHEDPEVKPMWYVDGVEVHNATKPREQYNSTYR 303
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 240 LFPKPKPDLMISRTPEVTCVVDVSHEDPEVKPMWYVDGVEVHNATKPREQYNSTYR 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 304 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISRAGQPREPQVYTLPPSRDELTKN 363
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 300 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISRAGQPREPQVYTLPPSRDELTKN 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 364 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGN 423
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQGN 419
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 424 VFSQSVHHEALHNHYTQKSLSLSPGK 449
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 420 VFSQSVHHEALHNHYTQKSLSLSPGK 445
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Search completed: December 23, 2004, 18:57:36
Job time : 160.692 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 23, 2004, 18:46:39 ; Search time 38.4376 Seconds
(without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071
Sequence: 1 EVGLVSGDFVPGGSLRV.....IVEFLNRWTFQSIISTLT 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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3: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2194.5	71.5	452	3	US-09-027-449-71 Sequence 71, Appl
2	2194.5	71.5	452	3	US-09-026-985-71 Sequence 71, Appl
3	2194.5	71.5	452	4	US-09-121-952A-71 Sequence 71, Appl
4	2194.5	71.5	452	4	US-09-234-340A-71 Sequence 71, Appl
5	2194.5	71.5	459	1	US-08-157-101A-7 Sequence 8, Appl1
6	2169	70.6	453	3	US-08-466-151-8 Sequence 8, Appl1
7	2169	70.6	453	3	US-08-466-163B-8 Sequence 8, Appl1
8	2169	70.6	453	4	US-09-802-096-8 Sequence 8, Appl1
9	2169	70.6	453	4	US-09-802-077-8 Sequence 8, Appl1
10	2167	70.6	451	2	US-08-887-352B-14 Sequence 14, Appl
11	2167	70.6	451	2	US-08-887-352B-16 Sequence 14, Appl
12	2167	70.6	451	3	US-08-466-151-65 Sequence 65, Appl
13	2167	70.6	451	3	US-09-109-207C-14 Sequence 14, Appl
14	2167	70.6	451	3	US-09-109-207C-16 Sequence 16, Appl
15	2167	70.6	451	3	US-09-286-005-14 Sequence 14, Appl
16	2167	70.6	451	3	US-09-286-005-16 Sequence 16, Appl
17	2167	70.6	451	4	US-09-920-171-14 Sequence 14, Appl
18	2167	70.6	451	4	US-09-920-171-16 Sequence 16, Appl
19	2167	70.6	451	4	US-09-716-028-14 Sequence 14, Appl
20	2167	70.6	451	4	US-09-716-028-16 Sequence 16, Appl
21	2167	70.6	451	4	US-10-113-996-14 Sequence 14, Appl
22	2167	70.6	451	4	US-10-113-996-16 Sequence 16, Appl
23	2163	70.4	451	2	US-08-887-352B-18 Sequence 18, Appl
24	2163	70.4	451	3	US-09-109-207C-18 Sequence 18, Appl
25	2163	70.4	451	3	US-09-109-207C-18 Sequence 18, Appl
26	2163	70.4	451	3	US-09-054-255-2 Sequence 2, Appl1
27	2163	70.4	451	3	US-09-296-005-18 Sequence 18, Appl

28	2163	70.4	451	4	US-09-282-846-2 Sequence 2, Appl1
29	2163	70.4	451	4	US-09-680-145-2 Sequence 2, Appl1
30	2163	70.4	451	4	US-09-920-171-18 Sequence 18, Appl
31	2163	70.4	451	4	US-09-716-028-18 Sequence 18, Appl
32	2163	70.4	451	4	US-09-483-588-2 Sequence 2, Appl1
33	2163	70.4	451	4	US-10-113-996-18 Sequence 18, Appl
34	2160.5	70.4	449	3	US-09-679-197-2 Sequence 2, Appl1
35	2160.5	70.4	449	3	US-09-680-148-2 Sequence 2, Appl1
36	2160.5	70.4	449	4	US-09-304-465A-2 Sequence 2, Appl1
37	2140	69.7	478	3	US-08-487-550-8 Sequence 8, Appl1
38	2140	69.7	478	4	US-09-526-098-8 Sequence 8, Appl1
39	2140	69.7	478	4	US-09-383-916-8 Sequence 13, Appl
40	2127	69.3	449	4	US-08-458-516-13 Sequence 42, Appl
41	2084.5	67.9	467	4	US-08-030-175-42 Sequence 90, Appl
42	2084	67.9	711	3	US-09-485-737B-90 Sequence 41, Appl
43	2081.5	67.8	467	4	US-08-030-175-41 Sequence 67, Appl
44	2081	67.8	468	3	US-09-485-737B-67 Sequence 10, Appl
45	2080	67.7	476	2	US-08-378-939-10

ALIGNMENTS

RESULT 1
US-09-027-449-71
Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leon, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-71
Query Match 71.5%; Score 2194.5; DB 3; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.3e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;

QY 1 EVOLVESGGDFVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
1 EVOLVSSGGGLVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
Db 1 EVOLVSSGGGLVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
QY 61 SDSVGRFTLSRDNKNTLYLQMSLRABDSAVYCTRYKL--GTYFDSMGQGLTV 117
61 NQKFKGRFTLSRDNKNTLYLQMSLRABDSAVYCTRYCARGDYRNGDWPFDMVQGLTV 120
Db 118 SSASTKGPVFLPAPSSKSTSGGTALGCLVNDYFPEPTVSMNSGALTSVHTTTPAVLQ 177
121 SSASTKGPVFLPAPSSKSTSGGTALGCLVNDYFPEPTVSMNSGALTSVHTTTPAVLQ 180
QY 178 SSGLSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVEPKSCDKHTTCCPAPPELL 237
181 SSGLSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVEPKSCDKHTTCCPAPPELL 240
QY 238 GGPVFLPFPKPKDMLTMRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREQ 297
241 GGPVFLPFPKPKDMLTMRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREQ 300
Db 298 YNSTRVSVLTVLHODMNLNGEKYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 357
301 YNSTRVSVLTVLHODMNLNGEKYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTPPVLDSDGSFFLYSKLTVDKS 417
361 EMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTPPVLDSDGSFFLYSKLTVDKS 420
Db 418 RMOQGNVFSQVMEHALNHHYTKSLSPGK 449
QY 421 RMOQGNVFSQVMEHALNHHYTKSLSPGK 452

RESULT 2
US-09-026-985-71
Sequence 71, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-026-985-71
Query Match 71.5%; Score 2194.5; DB 3; Length 452;
Best Local Similarity 90.9%; Pred. No. 2.3e-161;
Matches 411; Conservative 14; Mismatches 24; Indels 3; Gaps 1;
QY 1 EVOLVESGGDFVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
1 EVOLVSSGGGLVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
Db 1 EVOLVSSGGGLVQPGSLRVSCAAGFAPSHYAMSVROAPGKLEWVAIYSSGSGSTY 60
QY 61 SDSVGRFTLSRDNKNTLYLQMSLRABDSAVYCTRYKL--GTYFDSMGQGLTV 117
61 NQKFKGRFTLSRDNKNTLYLQMSLRABDSAVYCTRYCARGDYRNGDWPFDMVQGLTV 120
Db 61 NQKFKGRFTLSRDNKNTLYLQMSLRABDSAVYCTRYCARGDYRNGDWPFDMVQGLTV 120
QY 118 SSASTKGPVFLPAPSSKSTSGGTALGCLVNDYFPEPTVSMNSGALTSVHTTTPAVLQ 177
121 SSASTKGPVFLPAPSSKSTSGGTALGCLVNDYFPEPTVSMNSGALTSVHTTTPAVLQ 180
Db 121 SSASTKGPVFLPAPSSKSTSGGTALGCLVNDYFPEPTVSMNSGALTSVHTTTPAVLQ 180
QY 178 SSGLSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVEPKSCDKHTTCCPAPPELL 237
181 SSGLSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVEPKSCDKHTTCCPAPPELL 240
Db 181 SSGLSLSSVTVVPSSSLGTQTYICNVNKKPSNTKVDKVEPKSCDKHTTCCPAPPELL 240
QY 238 GGPVFLPFPKPKDMLTMRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREQ 297
241 GGPVFLPFPKPKDMLTMRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREQ 300
Db 241 GGPVFLPFPKPKDMLTMRTEPVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTKPREQ 300
QY 298 YNSTRVSVLTVLHODMNLNGEKYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 357
301 YNSTRVSVLTVLHODMNLNGEKYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 360
Db 301 YNSTRVSVLTVLHODMNLNGEKYKCKVSNKALPAPIETISKAKGQPREPOVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTPPVLDSDGSFFLYSKLTVDKS 417
361 EMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTPPVLDSDGSFFLYSKLTVDKS 420
Db 361 EMTKNQVSLTCLVKGFPYSDIAVEMESNGQEPENNYKTPPVLDSDGSFFLYSKLTVDKS 420
QY 418 RMOQGNVFSQVMEHALNHHYTKSLSPGK 449
Db 421 RMOQGNVFSQVMEHALNHHYTKSLSPGK 452

RESULT 3
US-09-121-952A-71
Sequence 71, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Haei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatohk, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:


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/ GENERAL INFORMATION:
/ APPLICANT: KURIHARA, TATSUYA
/ APPLICANT: MATSUKURA, SHIGEKAZU
/ APPLICANT: TSURUOKA, NOBUO
/ APPLICANT: ARIMA, KENJI
/ APPLICANT: NISHIHARA, TATSURO
/ TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
/ TITLE OF INVENTION: PLASMIDS THEREFOR
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: PILSBURY, MADISON & SUTRO
/ STREET: 1100 NEW YORK AVENUE, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/157,101A
/ FILING DATE: 05-APR-1994
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: TITUS, MARLANA K
/ REGISTRATION NUMBER: 35843
/ REFERENCE/DOCKET NUMBER: 9437/204199
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-861-3711
/ TELEFAX: 202-822-0944
/ TELEX: 6714627 CUCH
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 459 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-157-101A-7

Query Match          71.5%; Score 2194.5; DB 1; Length 459;
Best Local Similarity 91.8%; Pred. No. 2.3e-161;
Matches 413; Conservative 15; Mismatches 21; Indels 1; Gaps 1;

QY 1 EVOLVESGDFVQPGSLRVSCAASGFARSHYAMSVRQAPGKLEWVAIYSSGSGCTTY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10 QVQLVESGGGVVQPGKSLRLSCAASGFTPSNSMHWVRQAPGKLEWVAIVILDGNHKEY 69
QY 61 SDSVKGRFTISRDNSKNTLYLQWRSIPRADSAAVYFCTRVK-LGTYVPDSNGGTLTVSS 119
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 ADSVKGRTFISRDNSKNTLYLQWRSIPRADSAAVYFCTRVK-LGTYVPDSNGGTLTVSS 129
QY 120 ASTKGDSVPEPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
DB 130 ASTKGDSVPEPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 189
QY 180 GYSLSSVTVTVSSSGTGTQTYICNVNHRKSNTRVDDKVKPKSCDKHTGCPPCAAPFLDG 239
DB 190 GYSLSSVTVTVSSSGTGTQTYICNVNHRKSNTRVDDKVKPKSCDKHTGCPPCAAPFLDG 249
QY 240 PSVFLPEPPKDKTLMSRTPEVTQVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 299
DB 250 PSVFLPEPPKDKTLMSRTPEVTQVVDVSHEDPEVKFMVYDGVVHNAKTKPREEOYN 309
QY 300 STYRVVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPSRDE 359
DB 310 STYRVVSVLTVLHQMNLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPSRDE 369
QY 360 LTRKQVSLTCLVKGFPSPDIAYWESNGCPENNYKTTTPYLPDSGSPFLYSKLTVDKSW 419
DB 370 LTRKQVSLTCLVKGFPSPDIAYWESNGCPENNYKTTTPYLPDSGSPFLYSKLTVDKSW 429
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QY 420 QOQNVFSCSVMEALHNHYTQKSLSPGK 449
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
430 QOQNVFSCSVMEALHNHYTQKSLSPGK 459

RESULT 6
US-08-466-151-8
; Sequence 8, Application us/08466151
; Patent No. 6037453
/ GENERAL INFORMATION:
/ APPLICANT: Jardieu, Paula M.
/ APPLICANT: Presta, Leonard G.
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/466,151
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/466163
/ FILING DATE: 06-Jun-1995
/ APPLICATION NUMBER: 08/405617
/ FILING DATE: 15-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/185899
/ FILING DATE: 26-JAN-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/879495
/ FILING DATE: 07-MAY-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/744768
/ FILING DATE: 14-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Svoboda, Craig G.
/ REGISTRATION NUMBER: 39,044
/ REFERENCE/DOCKET NUMBER: P0718P2C1D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1489
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 453 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ US-08-466-151-8

Query Match          70.6%; Score 2169; DB 3; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.1e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;

QY 1 EVOLVESGDFVQPGSLRVSCAASGFARSHYAMSVRQAPGKLEWVAIYSSGSGCTTY 59
DB 1 EVOLVESGGGVVQPGKSLRLSCAASGFTPSNSMHWVRQAPGKLEWVAIVILDGNHKEY 59
QY 60 YDSVKGRTFISRDNSKNTLYLQWRSIPRADSAAVYFCTRVK-LGTYVPDSNGGTLTV 117
DB 60 YDSVKGRTFISRDNSKNTLYLQWRSIPRADSAAVYFCTRVK-LGTYVPDSNGGTLTV 119
QY 118 SGAFT-KQPSVFLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 175
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 120 SSASTKGGPSVFLPPLAPSSKSTSGCTAAGCLVADYFPEPVTVSWNSGALTSGVHTFPAY 179
Qy 176 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 235
Db 180 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 239
Qy 236 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 295
Db 240 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 299
Qy 296 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
Db 300 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 359
Qy 356 SRBELTKNOVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSGSPFLYSKLTVD 415
Db 360 SREEMTKNOVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSGSPFLYSKLTVD 419
Qy 416 KSRMOGNVFSQSVMEHALNHYTOKSLSPGK 449
Db 420 KSRMOGNVFSQSVMEHALNHYTOKSLSPGK 453

RESULT 7
US-08-466-163B-8
Sequence 8, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 453
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized maell, version 1 heavy chain
US-08-466-163B-8

Query Match 70.6%; Score 2169; DB 3; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.1e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;
Qy -
Db 1 EVOLVSSGGDFVQPGGSLRVSCAASGRF-SHYAMSVMVROAPKGLBVAIYSSGSGGT 59
Qy 60 YSDSVGRFTISDNRKNTLYLQMRSLRAEDSAVYFCTRVK--LGTVPFDSMGOGTLLTV 117
Db 60 YSDSVGRFTISDNRKNTLYLQMRSLRAEDTAIVYICAKSHYFGHMFVAVMGOGTLLTV 119
Qy 118 SSAST--KGPSVFLPPLAPSSKSTSGCTAAGCLVADYFPEPVTVSWNSGALTSGVHTFPAY 175
Db 120 SSASTKGGPSVFLPPLAPSSKSTSGCTAAGCLVADYFPEPVTVSWNSGALTSGVHTFPAY 179
Qy 176 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 235
Db 180 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 239
Qy 236 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 295

Db 240 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 299
Qy 296 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
Db 300 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 359
Qy 356 SRBELTKNOVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSGSPFLYSKLTVD 415
Db 360 SREEMTKNOVSLTCLVKGFPSPDIAYVESNGQPENNYKTTTPVLDSGSPFLYSKLTVD 419
Qy 416 KSRMOGNVFSQSVMEHALNHYTOKSLSPGK 449
Db 420 KSRMOGNVFSQSVMEHALNHYTOKSLSPGK 453

RESULT 8
US-09-802-096-8
Sequence 8, Application US/09802096
Patent No. 6685939
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
FILE REFERENCE: P0718P2C3US
CURRENT APPLICATION NUMBER: US/09/802,096
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 453
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-096-8

Query Match 70.6%; Score 2169; DB 4; Length 453;
Best Local Similarity 91.0%; Pred. No. 2.1e-159;
Matches 413; Conservative 16; Mismatches 19; Indels 6; Gaps 4;
Qy 1 EVOLVSSGGDFVQPGGSLRVSCAASGRF-SHYAMSVMVROAPKGLBVAIYSSGSGGT 59
Db 1 EVOLVSSGGGLVQPGGSLRVSCAVSGSITSGVSMWIRQAPKGLBVAIYDGS-TN 59
Qy 60 YSDSVGRFTISDNRKNTLYLQMRSLRAEDSAVYFCTRVK--LGTVPFDSMGOGTLLTV 117
Db 60 YSDSVGRFTISDNRKNTLYLQMRSLRAEDTAIVYICAKSHYFGHMFVAVMGOGTLLTV 119
Qy 118 SSAST--KGPSVFLPPLAPSSKSTSGCTAAGCLVADYFPEPVTVSWNSGALTSGVHTFPAY 175
Db 120 SSASTKGGPSVFLPPLAPSSKSTSGCTAAGCLVADYFPEPVTVSWNSGALTSGVHTFPAY 179
Qy 176 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 235
Db 180 LQSSGLYSLSVTVTVSSSLGTQTYICNVNHNKPSNTKVDKVEKSCDKHTHCPCPAPE 239
Qy 236 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 295
Db 240 LLAGPSVFLPFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNNYVADGEVHNAAKTKPRE 299
Qy 296 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
Db 300 EQNSTYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 359

[illegible]

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RESULT 9
US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. 6699472
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P011892C2US
; CURRENT FILING DATE: US/09/802.077
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: prt
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-09-802-077-8

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Query Match	70.6%	Score 2169	DB 4	Length 453
Best Local Similarity	91.0%	Prod. No. 2.1e-159		
Matches	413	Conservative	16	Mismatches 19
				Indels 6
				Gaps 4
Qy	1	EVOLVESGADPVQPGSGSLRVSCAASGFAP-SHYAMSWVRQAPGKGLEWVAVYISGGSGCTY	59	
Db	1	EVQLVESGGGLVQPGSGSLRLCAVSGYSITSGYSNMWIRQAQKGLIEWVASITYDGS-TN	59	
Qy	60	YDSYKGFITISRDNSKNTLYLQNRSLAEBSAYVFCIRVK--LCTYYPDSNGCCTLLTV	117	
Db	60	YADSKGFRFITSRDSSKNTFYLOMNSLAEETAYVYCARSGSHYFCHMWFAMWGGTILTV	119	
Qy	118	SSAST--KGPSVFLPAPSKSTSGGTALAGLVNDYFPEPTVSNNSGALTSGVHTPPAV	175	
Db	120	SSASTKGGPSVFLPAPSKSTSGGTALAGLVNDYFPEPTVSNNSGALTSGVHTPPAV	179	
Qy	176	LQSSGLYSLSASVYVPSSSLGTQYICNVNKKPSNTKYDKVPEKSCDKTHTCPCPAPE	235	
Db	180	LQSSGLYSLSASVYVPSSSLGTQYICNVNKKPSNTKYDKVPEKSCDKTHTCPCPAPE	239	
Qy	236	LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNAKTKRE	295	
Db	240	LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNAKTKRE	299	
Qy	296	EQNSYTVVSVLTALVHODMLNGEKYKCKVNSKALPAIEKTIISKAKQPREPOVYTLPP	355	
Db	300	EQNSTYVSVLTALVHODMLNGEKYKCKVNSKALPAIEKTIISKAKQPREPOVYTLPP	359	
Qy	356	SRDELTKQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPVLDSDGSFFLYSKLTV	415	
Db	360	SREEMTKQVSLTCLVKGFPYSDIAVEMESNGQEPNNYKTPPVLDSDGSFFLYSKLTV	419	
Qy	416	KSRMQGVSCSVMEHALAHNYTKSLISLSPK	449	

Db 420 KSRWQGGNVFSCSVMEALHNHYTQKSLSPGK 453

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1      RESULT 10
2      US-08-887-352B-14
3      ; Sequence 14, Application US/08887352B
4      ; Patent No. 5994511
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardine, John Lowe
7      ; TITLE OF INVENTION: Improved Anti-1GE Antibodies and Method of
8      ; TITLE OF INVENTION: Improving Polypeptides
9      ; NUMBER OF SEQUENCES: 26
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Genentech, Inc.
12     ; STREET: 1 DNA Way
13     ; CITY: South San Francisco
14     ; STATE: California
15     ; COUNTRY: USA
16     ; ZIP: 94080
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: Minipain (Genentech)
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/887,352B
24     ; FILING DATE: 03-Jul-1997
25     ; CLASSIFICATION: 530
26     ; ATTORNEY/AGENT INFORMATION:
27     ; NAME: Svoboda, Craig G.
28     ; REGISTRATION NUMBER: 39,044
29     ; REFERENCE/DOCKET NUMBER: P1123
30     ; TELECOMMUNICATION INFORMATION:
31     ; TELEPHONE: 650/225-1489
32     ; TELEFAX: 650/952-9881
33     ; INFORMATION FOR SEQ. ID NO: 14:
34     ; SEQUENCE CHARACTERISTICS:
35     ; LENGTH: 451 amino acids
36     ; TYPE: Amino Acid
37     ; TOPOLOGY: Linear
38     ; US-08-887-352B-14

```

[illegible]

QY 418 RMOQGNVFCSCVHHEALHNNHYTKSLSPGK 449
DB 420 RMOQGNVFCSCVHHEALHNNHYTKSLSPGK 451

RESULT 11

US-08-887-352B-16
Sequence 16, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-19S Antibodies and Method of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-16

Query Match 70.6%; Score 2167; DB 2; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVOLVSSGDDFVOPGSLRVSCAASGFAF-SHYAMSVMVROAPKGLFEMVAIYSSGGSGTY 59
DB 1 EVOLVSSGGGLVOPGSLRVSCAASGFAF-SHYAMSVMVROAPKGLFEMVAIYSSGGSGTY 59
QY 60 YSDSVKGRFTISRDNSKNTLYLQMRSILRAEDSAVYFCTRVK--LGTYYFDSWGOGLTLTV 117
DB 60 YNSVVGRTTISRDSKNTLYLQMRSILRAEDSAVYFCTRVK--LGTYYFDSWGOGLTLTV 119
QY 118 SSASTGSPVFPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALISGVTTPFAVLQ 177
DB 120 SSASTGSPVFPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALISGVTTPFAVLQ 179
QY 178 SSGLYSLSSVTVPPSSSLGQTYICVNNHPSNTYDKKVRPSCKTHPCPCPAPELL 237
DB 180 SSGLYSLSSVTVPPSSSLGQTYICVNNHPSNTYDKKVRPSCKTHPCPCPAPELL 239
QY 238 GGSVFLFPKPKDMLMISRTPEVTCVVDVSHEDDEVKFNMYVDGVEVNAATKPREQ 297
DB 240 GGSVFLFPKPKDMLMISRTPEVTCVVDVSHEDDEVKFNMYVDGVEVNAATKPREQ 299
QY 298 YNSTYVSVLYTLHODMLNGKEYKCKVSNKALPAPIEKTISPAKQPREPOVYTLPPSR 357
DB 300 YNSTYVSVLYTLHODMLNGKEYKCKVSNKALPAPIEKTISPAKQPREPOVYTLPPSR 359

QY 358 DELTKNOVSLTCLVKGFPYSDIAVEMESNQPENNYKTPPVLDSDGFFLYSKLTVDKS 417
DB 360 EEMTKNOVSLTCLVKGFPYSDIAVEMESNQPENNYKTPPVLDSDGFFLYSKLTVDKS 419
QY 418 RMOQGNVFCSCVHHEALHNNHYTKSLSPGK 449
DB 420 RMOQGNVFCSCVHHEALHNNHYTKSLSPGK 451

RESULT 12

US-08-466-151-65
Sequence 65, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAR-1992

NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-65

Query Match 70.6%; Score 2167; DB 3; Length 451;
Best Local Similarity 90.9%; Pred. No. 3e-159;
Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVOLVSSGDDFVOPGSLRVSCAASGFAF-SHYAMSVMVROAPKGLFEMVAIYSSGGSGTY 59
DB 1 EVOLVSSGGGLVOPGSLRVSCAASGFAF-SHYAMSVMVROAPKGLFEMVAIYSSGGSGTY 59
QY 60 YSDSVKGRFTISRDNSKNTLYLQMRSILRAEDSAVYFCTRVK--LGTYYFDSWGOGLTLTV 117
DB 60 YNSVVGRTTISRDSKNTLYLQMRSILRAEDSAVYFCTRVK--LGTYYFDSWGOGLTLTV 119

RESULT 15

US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 70.6%; Score 2167; DB 3; Length 451;

Best Local Similarity 90.9%; Pred. No. 3e-159;

Matches 411; Conservative 16; Mismatches 21; Indels 4; Gaps 3;

QY 1 EVOLVESGDVFVPGGSLRVSCAAGFAF-SHYAMSVVROAPGKLEWVAISSGSGTY 59
DB 1 EVOLVESGGLVPGGSLRLSCAVSGYISGYSWMNIRQAPGKLEWVASITYDGS-TN 59
QY 60 YSDSVGRFTISRDNSKNTLYIQWRSRAPDSAVYECTRVK--LGYTFPDSKGGTLLTV 117
DB 60 YNSVSKGRITISRDSDSKNTFYIQLWNLSLRADYAVYCARSGHYFGHWFAMWGQGLTV 119
QY 118 SSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPTVSNMNGALTSGVHFPAYLQ 177
DB 120 SSASTKGPVFPPLAPSSKSTSGTALGCLVKDYFPEPTVSNMNGALTSGVHFPAYLQ 179
QY 178 SSGLYSLSSVTVVPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKHTTCCPCPAPELL 237
DB 180 SSGLYSLSSVTVVPSSSLGTQTYICNVNHRPSNTKVDKVEPKSCDKHTTCCPCPAPELL 239
QY 238 GGSVFLFPKPKPDITLMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 297
DB 240 GGSVFLFPKPKPDITLMISRTPEYTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
QY 298 YNSTYRVSVLTLYHODMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 357
DB 300 YNSTYRVSVLTLYHODMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
QY 358 DELTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 417
DB 360 EEMTKQVSLTCLVKGFYPSDIAVEMESNQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
QY 418 RMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 449
DB 420 RMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 451

Search completed: December 23, 2004, 19:07:50
Job time : 40.4376 sec

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Qy	120	ISTGSESPPLA	BSKSTNSGCTAALG	CLVKDY	PRPVVUS	SMSGALTSGVHTPRAY	QSS	179																																															
Db	117	ASTKPSVPPLA	BSKSTNSGTAALG	CLVKDY	PRPVVUS	SMSGALTSGVHTPRAY	QSS	176																																															
Qy	180	GLYLS	SSVVV	VPSSSL	LGTYTY	ICNVH	KSPNTKVDK	EPKSPKSCDKHTCP	PCPAPELLG	239																																													
Db	177	GLYLS	SSVVV	TPSSSL	LGTYTY	ICNVH	KSPNTKVDK	RPVSPKSCDKHTCP	PCPAPELLG	236																																													
Qy	240	PSVFL	FPPEPKD	TLMI	SRTP	EVYTCVVVD	YSHED	PEYKFWY	YIDGVEV	HNAKTRREEQYN	239																																												
Db	237	PSVFL	FPPEPKD	TLMI	SRTP	EVYTCVVVD	YSHED	PEYKFWY	YIDGVEV	HNAKTRREEQYN	236																																												
Qy	300	STYRV	SV	YLT	VL	YHQM	LNK	EYKCYK	CKVSN	ALPAPI	EKITSKAKGQ	PREPOVYTL	PPSRRE	359																																									
Db	297	STYRV	SV	YLT	VL	YHQM	LNK	EYKCYK	CKVSN	ALPAPI	EKITSKAKGQ	PREPOVYTL	PPSRRE	356																																									
Qy	360	LTKNO	VS	LT	CLV	KGY	PSD	IA	VEB	SNQ	PENN	YKTP	PVL	DSG	FPLY	SKLTV	DKSRW	419																																					
Db	357	MTKNO	VS	LT	CLV	KGY	PSD	IA	VEB	SNQ	PENN	YKTP	PVL	DSG	FPLY	SKLTV	DKSRW	416																																					
Qy	420	QOGN	V	FS	C	SV	HEA	L	NH	Y	T	O	K	S	L	S	P	E	K	A	P	T	S	S	T	K	T	O	L	E	H	L	L	D	Q	M	I	L	G	I	N	N	479												
Db	417	QOGN	V	FS	C	SV	HEA	L	NH	Y	T	O	K	S	L	S	P	E	K	A	P	T	S	S	T	K	T	O	L	E	H	L	L	D	Q	M	I	L	G	I	N	N	476												
Qy	480	YKNP	KL	TE	M	L	T	E	K	F	Y	M	P	K	K	A	T	E	L	K	H	L	Q	C	E	B	E	L	K	P	L	E	B	V	L	N	A	Q	S	R	N	F	H	L	R	P	R	D	L	I	S	N	I	N	539
Db	477	YKNP	KL	TE	M	L	T	E	K	F	Y	M	P	K	K	A	T	E	L	K	H	L	Q	C	E	B	E	L	K	P	L	E	B	V	L	N	A	Q	S	R	N	F	H	L	R	P	R	D	L	I	S	N	I	N	536
Qy	540	VIV	EL	K	G	S	E	T	T	F	M	C	E	Y	A	D	E	T	A	I	Y	E	F	L	R	M	W	I	T	F	C	O	S	I	I	S	T	L	T	582															
Db	537	VIV	EL	K	G	S	E	T	T	F	M	C	E	Y	A	D	E	T	A	I	Y	E	F	L	R	M	W	I	T	F	C	O	S	I	I	S	T	L	T	579															

RESULT 2
 US-10-310-719-32
 Sequence 32, Application US/10310719
 Publication No. US20030166153A1
 GENERAL INFORMATION:
 APPLICANT: Gililee, Stephen
 TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
 FILE REFERENCE: Lex-020
 CURRENT APPLICATION NUMBER: US/10/310, 719
 CURRENT FILING DATE: 2002-12-04
 PRIOR APPLICATION NUMBER: 60/337, 113
 PRIOR FILING DATE: 2001-12-04
 PRIOR APPLICATION NUMBER: 60/371, 966
 PRIOR FILING DATE: 2002-04-12
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 32
 LENGTH: 579
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
 US-10-310-719-32

Query Match	89.6%	Score 2750.5;	DB 14;	Length 579;
Best Local Similarity	88.5%;	Pred. No. 8.2e-166;		
Matches 516;	Conservative 32;	Mismatches 30;	Indels 5;	Gaps 2

QY 1 EVLVESGGDPVQPGSGSLRVSCAAGFAISHYAMSVRQAPGKGLMVAIYSSGGSGITY 60
Db 1 QIOLQSPPELKKPSSSVKISCKASGYTLTNGMNVRAQPGKGLMGMINTYGEPTY 60
QY 61 SDSVGRPTLSRDNKNLTLYLQMRSLRAEDSAVYFCTR-VKLGITYFPDSMGQTLTVSS 119
Db 61 ADDEGGRPTLTAEISTSTLYLQLNLMRSDEPTATYFCVREISKXDY----WGQETVTVSS 116
QY 120 ASTKSPSPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSNMNGALTSQGHTEPAVLQSS 179
Db 117 ASTKSPSPVPLAPSSKSTSGTAALGCLVKDYFPEPVTVSNMNGALTSQGHTEPAVLQSS 176

Qy	180	LLSLSSLVVTVPPSSSLGQVOTI CANNHNRPNKVDKXVPEKSCDHTHTPCPCAPELLGG	239
Db	177	GLTSLSSVTVTVPPSSSLGTQVYI CANNHNRPNKVKVPEKSCDKHTHTPCPCAPELLGG	236
Qy	240	PSVFLPEPKPDYTLMI SRTPEVTCVVVDVSHEDPEVKFMVYDGVGEVHNAKTPPREQYN	299
Db	237	PSVFLPEPKPDYTLMI SRTPEVTCVVVDVSHEDPEVKFMVYDGVGEVHNAKTPPREQYN	296
Qy	300	STYRVSVLTVLHODMILNGKEYCKCVSNKALPAPI EKTISKAKGQPREPOVYTLPPSRDE	359
Db	297	STYRVSVLTVLHODMILNGKEYCKCVSNKALPAPI EKTISKAKGQPREPOVYTLPPSRDE	356
Qy	360	LTKNOVSLTLCVKGGYPSDIAVEMESNQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRM	419
Db	357	MTKNOVSLTLCVKGGYPSDIAVEMESNQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRM	416
Qy	420	QOQGNVFCSVVHEALHNHYTQKSLSLSPGKAPTSSSTKTKQLQL EHLILLDLOMILNGINN	479
Db	417	QOQGNVFCSVVHEALHNHYTQKSLSLSPGKAPTSSSTKTKQLQL EHLILLDLOMILNGINN	476
Qy	480	YKNPKLTMLTFFKFMYPKKATELKLHQLCEBELKPLEEVLNLAQSKNFKLRPDLISINN	539
Db	477	YKNPKLTMLTFFKFMYPKKATELKLHQLCEBELKPLEEVLNLAQSKNFKLRPDLISINN	536
Qy	540	VIVLELKSESTTFPMCEYADETRATIEYFLNRTWTFQOSIISTLT	582
Db	537	VIVLELKSESTTFPMCEYADETRATIEYFLNRTWTFQOSIISTLT	579

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RESULT 3
US-10-737-208A-6
/ Sequence 6, Application US/10737208A
/ Publication No. US20040203100A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen D.
/ APPLICANT: Lo, Kin-Ming
/ TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
/ FILE REFERENCE: LEX-023
/ CURRENT APPLICATION NUMBER: US/10/737,208A
/ CURRENT FILING DATE: 2003-12-16
/ PRIOR APPLICATION NUMBER: US 60/433,945
/ PRIOR FILING DATE: 2002-12-17
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 575
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-II-2
US-10-737-208A-6

```

Query Match	88.6%	Score 2719.5;	DB 17;	Length 575;
Best Local Similarity	89.0%;	Pred. No. 7.4e-164;		
Matches 518;	Conservative 24;	Mismatches 33;	Indels 7;	Gaps 3

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QY 1 EVOLVLESSGDDVVOGCGSLRVCGASGAFPSHYAMWMTQA PCKGLIEMVAIVSSGSGCTYY 60
Db 1 EVQLVQSSAEAEKPKAPSAVKISCKASGSSPTGNMNMVVRONIKSLIEMICAIADIPYGGTISY 60
QY 61 SDSVKGREFTIIRDNSKNTLYLQMSIARAEDSAVVECTVKLGTYFYFDSWGQGTLLTVSSA 120
Db 61 NQKRGKRTILTVNDKSTSTAYMHKLKSLREDPAIVVYCVS---GMEY---WGQGSVTVSSA 114
QY 121 STKGDSVFPPLAPSSKSTISGCTPALGCLVKDYFPEPVTVSWNSGALTSGVHTPPAVLQSSG 180
Db 115 STKGDSVFPPLAPSSKSTISGCTPALGCLVKDYFPEPVTVSWNSGALTSGVHTPPAVLQSSG 174
QY 181 LYSLSAVTVTVSSLSIGTQTYICNVNKKRSNTVDDKKVPEKSCDCKHTPCPCPAPELLGCP 240
Db 175 LYSLSAVTVTVSSLSIGTQTYICNVNKKRSNTVDDKKVPEKSCDCKHTPCPCPAPELLGCP 234
QY 241 SVFLPEPKPKDQLMISRTPEVTVCVVVDVSDHEDPEYKFNMYVDGVGEVHNAKTKRREQVNS 300

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Db 235 SVFLPPKPKDITLMISTPEVTCVVVDVSHEDPEVKNNVYDGEVHNATKTPREEDYN 294
Qy 301 TYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSDEL 360
Db 295 TYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSHEM 354
Qy 361 TKNOVSLTCLVAGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSKRW 420
Db 355 TKNOVSLTCLVAGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSKRW 414
Qy 421 QGNVSCSVHAEALHNHYTQKSLSLSPGKAPTSSTTKTQLOLEHLLDLOMILNINN 480
Db 415 QGNVSCSVHAEALHNHYTQKSLSLSPGKAPTSSTTKTQLOLEHLLDLOMILNINN 473
Qy 481 KNPRLTRMLTFKFPYMPKATELKHQCLEBEELKPLEEVNLNLAOSKNFHLPRDLISNIN 540
Db 474 KNPRLTRMLTFKFPYMPKATELKHQCLEBEELKPLEEVNLNLAOSKNFHLPRDLISNIN 533
Qy 541 VIVLELKGSETTFMCEYADETATIVFELNRMITFCOSIISTLT 582
Db 534 VIVLELKGSETTFMCEYADETATIVFELNRMITFCOSIISTLT 575

RESULT 4
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines with Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310, 719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; LENGTH: 580
; SEQ ID NO 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NH576 (gamma4h) (FN>AQ)-ala-IL2 (D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match 85.3%; Score 2621; DB 14; Length 580;
Best Local Similarity 85.8%; Pred. No. 1.3e-157;
Matches 500; Conservative 29; Mismatches 50; Indels 4; Gaps 3;
Qy 1 EVOLVSGDGFVOPGSGILRVSCAASGAFASH-YAMSVNRQAPGKGLWVAIYSSGSGTY 59
Db 1 QVQLQESGGGLVAPSETLSLTCAVSGYSISGYYWGIKQPPKGLWGISITHSQS-ty 59
Qy 60 YSDSVKGRFTISRDNSKNTLYLQMNSLRADSAVYFCTRYKLTGYVFDWGQGTLLTVSS 119
Db 60 YNSLSKRYTISVDTSKNOFSLKLSSTVADTAIVYCARGRMSK--FDYWGQGTLLTVSS 117
Qy 120 ASTGKSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 118 ASTGKSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
Qy 180 GLYSLSVTVTPSSSLGTQTYICNNVHNPSTKVDKVEPKSCDKHTHCPCPAPAEFLG 239
Db 178 GLYSLSVTVTPSSSLGTQTYICNNVHNPSTKVDKVEPKSCDKHTHCPCPAPAEFLG 237
Qy 240 PSVFLPPKPKDITLMISTPEVTCVVVDVSHEDPEVKNNVYDGEVHNATKTPREEDYN 299
Db 238 PSVFLPPKPKDITLMISTPEVTCVVVDVSHEDPEVKNNVYDGEVHNATKTPREEDYN 297

Qy 300 STYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSDE 359
Db 298 STYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSDE 357
Qy 360 LTRNOVSLTCLVAGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSKRW 419
Db 358 LTRNOVSLTCLVAGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSKRW 417
Qy 420 QGNVSCSVHAEALHNHYTQKSLSLSPGKAPTSSTTKTQLOLEHLLDLOMILNINN 479
Db 418 QGNVSCSVHAEALHNHYTQKSLSLSPGKAPTSSTTKTQLOLEHLLDLOMILNINN 477
Qy 480 KNPRLTRMLTFKFPYMPKATELKHQCLEBEELKPLEEVNLNLAOSKNFHLPRDLISNIN 539
Db 478 KNPRLTRMLTFKFPYMPKATELKHQCLEBEELKPLEEVNLNLAOSKNFHLPRDLISNIN 537
Qy 540 VIVLELKGSETTFMCEYADETATIVFELNRMITFCOSIISTLT 582
Db 538 VIVLELKGSETTFMCEYADETATIVFELNRMITFCOSIISTLT 580

RESULT 5
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines with Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310, 719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NH576 (gamma2h) (FN>AQ)-ala-IL2 (D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
US-10-310-719-35

Query Match 84.3%; Score 2589; DB 14; Length 580;
Best Local Similarity 85.1%; Pred. No. 1.4e-155;
Matches 497; Conservative 29; Mismatches 52; Indels 6; Gaps 5;
Qy 1 EVOLVSGDGFVOPGSGILRVSCAASGAFASH-YAMSVNRQAPGKGLWVAIYSSGSGTY 59
Db 1 QVQLQESGGGLVAPSETLSLTCAVSGYSISGYYWGIKQPPKGLWGISITHSQS-ty 59
Qy 60 YSDSVKGRFTISRDNSKNTLYLQMNSLRADSAVYFCTRYKLTGYVFDWGQGTLLTVSS 119
Db 60 YNSLSKRYTISVDTSKNOFSLKLSSTVADTAIVYCARGRMSK--FDYWGQGTLLTVSS 117
Qy 120 ASTGKSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
Db 118 ASTGKSPVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
Qy 179 SGLYSLSVTVTPSSSLGTQTYICNNVHNPSTKVDKVEPKSCDKHTHCPCPAPAEFLG 238
Db 178 SGLYSLSVTVTPSSSLGTQTYICNNVHNPSTKVDKVEPKSCDKHTHCPCPAPAEFLG 236
Qy 239 GRSVFLPPKPKDITLMISTPEVTCVVVDVSHEDPEVKNNVYDGEVHNATKTPREEDYN 298
Db 237 GRSVFLPPKPKDITLMISTPEVTCVVVDVSHEDPEVKNNVYDGEVHNATKTPREEDYN 296
Qy 299 NSTYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSD 358
Db 297 NSTYRVSVVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGPREPOVYTLPPSD 356

QY	359	ELTKNQVSLTCLVNGFYPSDIAVEMESNGPENNYKTPPLVLDGSGFFLXSKLTIVKSR	418
Db	357	EMTKNQVSLTCLVNGFYPSDIAVEMESNGPENNYKTPPLVLDGSGFFLXSKLTIVDSR	416
QY	419	WQGVNFSQSVWHEALHNHYQKSLSLSPGKAPLTSSSTKTKTOLQLEHLLLDLQMLINGIN	478
Db	417	WQGVNFSQSVWHEALHNHYQKSLSLSPGKAPLTSSSTKTKTOLQLEHLLLDLQMLINGIN	476
QY	479	NYKPKLTLMLTFKKYMPKKAATELKHLOCLBEELKPLEEVLNLAOSKXPHLRPDLISNI	538
Db	477	NYKPKLTLMLTFKKYMPKKAATELKHLOCLBEELKPLEEVLNLAOSKXPHLRPDLISNI	536
QY	539	NYVLELKGSETTFMCEYADEPATVFEPLNMTFPCOSIISLT	582
Db	537	NYVLELKGSETTFMCEYADEPATVFEPLNMTFPCOSIISLT	580
RESULT 6			
US-10-474-832-4			
; Sequence 4, Application US/10474832			
; Publication No. US20040081651A1			
; GENERAL INFORMATION:			
; APPLICANT: BIOGEN, INC.			
; TITLE OF INVENTION: ANTIBODIES TO VLA-1			
; FILE REFERENCE: A101 PCT			
; CURRENT APPLICATION NUMBER: US/10/474,832			
; CURRENT FILING DATE: 2003-10-14			
; PRIOR APPLICATION NUMBER: 60/283,794			
; PRIOR FILING DATE: 2001-04-13			
; PRIOR APPLICATION NUMBER: 60/303,689			
; PRIOR FILING DATE: 2001-07-06			
; NUMBER OF SEQ ID NOS: 70			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 4			
; LENGTH: 447			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
; OTHER INFORMATION: polypeptide			
US-10-474-832-4			
Query Match 73.2%; Score 2246.5; DB 15; Length 447;			
Best Local Similarity 95.1%; Pred. No. 4,8e-134;			
Matches 426; Conservative 4; Mismatches 17; Indels 1; Gaps 1;			
QY	1	EVQLVESGGDLYQPGGSLRVSCHASGFRFSHYANSWFOAPQKGLIEWTAIYISGGSGTYY	60
Db	1	EVQLVESGGGIVQPGGSLRLSCASGFTFSRYTMSWVAQAGKGLIEWALTISGGH-TYY	59
QY	61	SDSVYGRFTISRDNSKNTLYIQMDSLRSEDSAVYFCRFVKLGITYYFDSMGSTLLTVSSA	120
Db	60	LDVYGRFTTISRDNKNTLYIQMDSLRSEDTAVYICRFGDGYYFDWGGSTLLTVSSA	119
QY	121	STKGPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPEVTVSNWSGALTSGVHTFPAVLQSSG	180
Db	120	STKGPSVPEPLAPSSKSTSGTAALGCLVKDYFPEPEVTVSNWSGALTSGVHTFPAVLQSSG	179
QY	181	LYSLSAVTVTVSSISGTTQYICNVNHNKSNSTKVDKVPKSCDKTHTCPCPAPELLGGP	240
Db	180	LYSLSAVTVTVSSISGTTQYICNVNHNKSNSTKVDKVPKSCDKTHTCPCPAPELLGGP	239
QY	241	SVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDVGVEVHNAKTKPREQYNS	300
Db	240	SVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDVGVEVHNAKTKPREQYNS	299
QY	301	TYRIVSVTLTVLHQMVLNKGKCYKSNKALPAPIEKTIKAKGQPREPOVYTLPPSRDEL	360
Db	300	TYRIVSVTLTVLHQMVLNKGKCYKSNKALPAPIEKTIKAKGQPREPOVYTLPPSRDEL	359
QY	361	TKNQVSLTCLVNGFYPSDIAVEMESNGPENNYKTPPLVLDGSGFFLXSKLTIVDKSWQ	420

Db	360	TKNQVSLTCLVKGYRPSDIAVENMSNQPENNYKTTTPVLDSDSGFFLYSKLTVDKSRMQ	418
Qy	421	QGAVFSCSVMEALHNHYTKSLSLSPG	448
Db	420	QGAVFSCSVMEALHNHYTKSLSLSPG	447

RESULT 7
US-10-474-832-5
; Sequence 5, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
 APPLICANT: BIOGEN, INC.
 TITLE OF INVENTION: ANTIBODIES TO VLA-1
 FILE REFERENCE: A101 PCT
 CURRENT APPLICATION NUMBER: US/10/474,832
 CURRENT FILING DATE: 2003-10-14
 PRIOR APPLICATION NUMBER: 60/289,794
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/303,689
 PRIOR FILING DATE: 2001-07-06
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 5
 LENGTH: 447
 TYPE: PRT
 ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-474-832-5

Query Match	73.0%; Score 2240.5; DB 15; Length 447;
Best Local Similarity	94.9%; Pred. No. 1.1e-133;
Matches 425; Conservative 4; Mismatches 18; Indels 1; Gaps 1;	

Qy	1	EVOLVESGDPRVOGGSGIRVSCASGFASFHYAMSWRQAAPGKLEWAVYISGSGSYTY	60
Db	1	EVLIVESGGGLVQGGSGLRISCASGFTFSRYTSWRQAAGKLEWATISGGGH-TYY	59
Qy	61	SDSVKGRFTISRDNRSKNTLYIQMNSLRADSAVVFCTRVKLGTTFYPDSMGQTLLTVSSA	120
Db	60	LDSVKAGRFTISRDNRSKNTLYIQMNSLRADPAVAYCYTRGPDDGTFPDWGQTLVTYSSA	119
Qy	121	STKGPSVEFLPAPSSKSITSGGTAAIGCVKDYPPEPVTVSNMSGALTSGVHTFPAYLOS	180
Db	120	STKGPSVEPLAPSSKITSSTGTAAIGCVKYDFPEPVTVSNMSGALTSGVHTFPAYLOS	179
Qy	181	LYSLSSVTVVSSLSIGTOTYICNNNHRPSNTKVDPKSEPCDTHHCCPPAPAEILGCP	240
Db	180	LYSLSSVTVVSSLSIGTOTYICNNNHRPSNTKVDPKSEPCDTHHCCPPAPAEILGCP	239
Qy	241	SVFLPFPKPCKDTLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKEPREOYNS	300
Db	240	SVFLPFPKPCKDTLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKEPREOYNS	299
Qy	301	TYRIVSVLTVLHQDWLNGKEYKCVRYSKKALPAPIEKTIISAKGQPREPQVYTTLPSSDEL	360
Db	300	TYRIVSVLTVLHQDWLNGKEYKCVRYSKKALPAPIEKTIISAKGQPREPQVYTTLPSSDEL	359
Qy	361	TKNOVSILTCLVKGYRPSDIAVENMSNQPENNYKTTTPVLDSDSGFFLYSKLTVDKSRMQ	420
Db	360	TKNOVSILTCLVKGYRPSDIAVENMSNQPENNYKTTTPVLDSDSGFFLYSKLTVDKSRMQ	419
Qy	421	QGAVFSCSVMEALHNHYTKSLSLSPG	448
Db	420	QGAVFSCSVMEALHNHYTKSLSLSPG	447

RESULT 8
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1

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; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-412-406-32

Query Match          72.9%; Score 2238.5; DB 15; Length 663;
Best Local Similarity 94.0%; Pred. No. 2.4e-133;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAASGAFSHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 215 EVOLVSGGGLVPRGSLRLSCAASGFTSDYMYWRQAPGKLEWVAIISDGSTYY 274
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDVKGKFTISRNSKNTLYLQMSLRABDSAVYFCTRYKLG-YYFDSWGQGLTLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 275 PDSVKGRFTISRNNKNSLYLQMSLRABDTAVYYCARBENGNYFYFDYWGQGLTVTVSS 334
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 ASTKGPSVFPFLAPSSKSTSGTALGCLVVDYFPEPTVSMNSGALTSGVHTFPAYLQSS 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 335 ASTKGPSVFPFLAPSSKSTSGTALGCLVVDYFPEPTVSMNSGALTSGVHTFPAYLQSS 394
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHCPCPAPELLGG 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 395 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHCPCPAPELLGG 454
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 PSYFLPPPKKDTLMSRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREBQYN 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 455 PSYFLPPPKKDTLMSRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREBQYN 514
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 STTRVSVTLTVLHQMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 515 STTRVSVTLTVLHQMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 574
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 LTRNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 419
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 575 LTRNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 634
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 QCGNVFSCSVMEHALHNHYTQKSLSPG 448
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 635 QCGNVFSCSVMEHALHNHYTQKSLSPG 663
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
; US-10-412-406-33
; Sequence 33, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: GARBER, Ellen
; APPLICANT: LYNE, Paul
; APPLICANT: SALDHANA, Jose W.
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
; FILE REFERENCE: BINA100CN
```

```

; CURRENT APPLICATION NUMBER: US/10/412,406
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 60/240,285
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/275,289
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/299,987
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/US01/32140
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4852
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-412-406-33

Query Match          72.9%; Score 2238.5; DB 15; Length 4852;
Best Local Similarity 94.0%; Pred. No. 2.5e-132;
Matches 422; Conservative 8; Mismatches 18; Indels 1; Gaps 1;

QY 1 EVOLVSGGDFVPGGSLRVSCAASGAFSHYAMSVWRQAPGKLEWVAIYSSGSGSTYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4404 EVOLVSGGGLVPRGSLRLSCAASGFTSDYMYWRQAPGKLEWVAIISDGSTYY 4463
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDVKGKFTISRNSKNTLYLQMSLRABDSAVYFCTRYKLG-YYFDSWGQGLTLTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4464 PDSVKGRFTISRNNKNSLYLQMSLRABDTAVYYCARBENGNYFYFDYWGQGLTVTVSS 4523
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 ASTKGPSVFPFLAPSSKSTSGTALGCLVVDYFPEPTVSMNSGALTSGVHTFPAYLQSS 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4524 ASTKGPSVFPFLAPSSKSTSGTALGCLVVDYFPEPTVSMNSGALTSGVHTFPAYLQSS 4583
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHCPCPAPELLGG 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4584 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTHCPCPAPELLGG 4643
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 PSYFLPPPKKDTLMSRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREBQYN 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4644 PSYFLPPPKKDTLMSRTPETVCVVVDVSHEDPEVKFNMYVDGVEVHNAKTPREBQYN 4703
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 STTRVSVTLTVLHQMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4704 STTRVSVTLTVLHQMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 4763
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 LTRNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 419
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4764 LTRNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPVLDSGSEFLYSKLTVDKSRW 4823
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 QCGNVFSCSVMEHALHNHYTQKSLSPG 448
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 4824 QCGNVFSCSVMEHALHNHYTQKSLSPG 4852
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
; US-10-474-832-6
; Sequence 6, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; FILE REFERENCE: A101 PCT
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 447
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-10-474-832-6
```

```

Query Match          72.8%; Score 2236.5; DB 15; Length 447;
Best Local Similarity 94.6%; Pred. No. 2.1e-133;
Matches 424; Conservative 4; Mismatches 19; Indels 1; Gaps 1;
```

```

QY 1 EVQLVESGGD FVQPGSGLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVA YISGGSGITYY 60
   |||||
DB 1 EVQLVESGGGALVQPGSGLRSLSCAASGFTFSRYTMSWVRQAPGKGLEWVA YISGGSGH-ITY 59
   |||||

QY 61 SDSVKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 120
   |||||
DB 60 LQSVKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 119
   |||||

QY 121 STKGSPVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
   |||||
DB 120 STKGSPVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 179
   |||||

QY 181 LYSLSVTVTPSSSLGTQTYICNVNHPSENTRYDKKVEPKSCDKHTTCCPPAPPELLGGP 240
   |||||
DB 180 LYSLSVTVTPSSSLGTQTYICNVNHPSENTRYDKKVEPKSCDKHTTCCPPAPPELLGGP 239
   |||||

QY 241 SYFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTREQYNSTR 300
   |||||
DB 240 SYFLPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTREQYNSTR 299
   |||||

QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
   |||||
DB 300 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 359
   |||||

QY 361 TRKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 420
   |||||
DB 360 TRKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQ 419
   |||||

QY 421 QGNVFSCSVMEHALHNHYTQKSLSPG 448
DB 420 QGNVFSCSVMEHALHNHYTQKSLSPG 447
```

```

RESULT 11
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US2003019405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79
```

```

Query Match          72.8%; Score 2234.5; DB 14; Length 445;
Best Local Similarity 94.4%; Pred. No. 2.7e-133;
Matches 421; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
```

```

QY 4 LVEGGD FVQPGSGLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVA YISGGSGITYYSDS 63
   |||||
DB 1 LVEGGGALVQPGSGLRSLSCAASGFTFSRYTMSWVRQAPGKGLEWVA YISGGSGITYYADS 60
   |||||

QY 64 VKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 123
   |||||
DB 61 VKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 119
   |||||

QY 124 GPSVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
   |||||
DB 120 GPSVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 179
   |||||

QY 184 LSSVTVTPSSSLGTQTYICNVNHPSENTRYDKKVEPKSCDKHTTCCPPAPPELLGGP 243
   |||||
DB 180 LSSVTVTPSSSLGTQTYICNVNHPSENTRYDKKVEPKSCDKHTTCCPPAPPELLGGP 239
   |||||

QY 244 LFPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTREQYNSTR 303
   |||||
DB 240 LFPPPKKDTLMTSRPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTREQYNSTR 299
   |||||

QY 304 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 363
   |||||
DB 300 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 359
   |||||

QY 364 QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQGN 423
   |||||
DB 360 QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRMQGN 419
   |||||

QY 424 VFSCSVMEHALHNHYTQKSLSPG 449
DB 420 VFSCSVMEHALHNHYTQKSLSPG 445
```

```

RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody B1M4 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6
```

```

Query Match          72.7%; Score 2231.5; DB 14; Length 444;
Best Local Similarity 93.8%; Pred. No. 4.2e-133;
Matches 421; Conservative 10; Mismatches 13; Indels 5; Gaps 1;
```

```

QY 1 EVQLVESGGD FVQPGSGLRVSCAASGFAFSHYAMSWVRQAPGKGLEWVA YISGGSGITYY 60
   |||||
DB 1 EVQLVESGGGALVQPGSGLRSLSCAASGFTFSRYTMSWVRQAPGKGLEWVA YISGGSGITYY 60
   |||||

QY 61 SDSVKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 120
   |||||
DB 61 SDSVKGRFTISRDNKNTLYIQMNSLRADDAVYCTRGFGDGCPDVMGQGLTVTVSSA 115
   |||||

QY 121 STKGSPVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
   |||||
DB 116 STKGSPVFPPLAPSSKSTSGGTAALGCLVADYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 175
   |||||

QY 181 LYSLSVTVTPSSSLGTQTYICNVNHPSENTRYDKKVEPKSCDKHTTCCPPAPPELLGGP 240
   |||||
```

Db 176 LYSLSAVVTVPPSSSLGTQTYICVNNHKSNTKVDKKEPKSCDTHTCPCPAPBELLGCP 235
QY 241 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 300
Db 236 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 295
QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 360
Db 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 355
QY 361 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 420
Db 356 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 415
QY 421 QGNVFCSCVMHEALHNHYTQKSLSPGK 449
Db 416 QGNVFCSCVMHEALHNHYTQKSLSPGK 444

RESULT 13

US-10-704-522-6
; Sequence 6, Application US/10704522
; Publication No. US20040120949A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baumann, Michael
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and methods for treating cancer using
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BiWA 4 Heavy Chain
US-10-704-522-6

Query Match 72.7%; Score 2231.5; DB 16; Length 444;

Best Local Similarity 93.8%; Pred. No. 4.2e-133;
Matches 421; Conservative 10; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKGLEWVAIVSSGSGTTY 60
Db 1 EVQLVESGGDLVPRGGSRLRSCTAASGFTFSYDMSWVROAPGKGLEWVSTISSGSGTTY 60
QY 61 SDVKGKFTISRDNKSKTLYLQWRSLRAEDSAVYFCTRYVLTGYTFPSMGQTLTVSSA 120
Db 61 LDSIKGFRTISRDNKSKTLYLQWRSLRAEDSAVYFCTRYVLTGYTFPSMGQTLTVSSA 115
QY 121 STGSPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSG 180
Db 116 STGSPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSG 175
QY 181 LYSLSAVVTVPPSSSLGTQTYICVNNHKSNTKVDKKEPKSCDTHTCPCPAPBELLGCP 240
Db 176 LYSLSAVVTVPPSSSLGTQTYICVNNHKSNTKVDKKEPKSCDTHTCPCPAPBELLGCP 235
QY 241 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 300
Db 236 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 295
QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 360

Db 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 355
QY 361 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 420
Db 356 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 415
QY 421 QGNVFCSCVMHEALHNHYTQKSLSPGK 449
Db 416 QGNVFCSCVMHEALHNHYTQKSLSPGK 444

RESULT 14

US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BiWA 4 Heavy Chain
US-10-645-215-6

Query Match 72.7%; Score 2231.5; DB 16; Length 444;

Best Local Similarity 93.8%; Pred. No. 4.2e-133;
Matches 421; Conservative 10; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVQLVESGGDFVPGGSLRVSCAASGFAFSHYAMSWVROAPGKGLEWVAIVSSGSGTTY 60
Db 1 EVQLVESGGDLVPRGGSRLRSCTAASGFTFSYDMSWVROAPGKGLEWVSTISSGSGTTY 60
QY 61 SDVKGKFTISRDNKSKTLYLQWRSLRAEDSAVYFCTRYVLTGYTFPSMGQTLTVSSA 120
Db 61 LDSIKGFRTISRDNKSKTLYLQWRSLRAEDSAVYFCTRYVLTGYTFPSMGQTLTVSSA 115
QY 121 STGSPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSG 180
Db 116 STGSPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQSSG 175
QY 181 LYSLSAVVTVPPSSSLGTQTYICVNNHKSNTKVDKKEPKSCDTHTCPCPAPBELLGCP 240
Db 176 LYSLSAVVTVPPSSSLGTQTYICVNNHKSNTKVDKKEPKSCDTHTCPCPAPBELLGCP 235
QY 241 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 300
Db 236 SVFLPPPKPDOTLMISTPEVTCVVDVSHEDPEVKFNWYDGEVHNATKPREEOYNS 295
QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 360
Db 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 355
QY 361 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 420
Db 356 TKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPVLDSDGSFPLYSKLTVDSKRWQ 415
QY 421 QGNVFCSCVMHEALHNHYTQKSLSPGK 449

Db 416 QGNVFSQSVMEALHNHYTQKSLSPGK 444

RESULT 15

US-09-736-371B-21
; Sequence 21, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
; CURRENT APPLICATION NUMBER: US/09/736,371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909, 8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-371B-21

Query Match

72.5%; Score 2226; DB 9; Length 449;

Best Local Similarity 93.1%; Pred. No. 9.5e-133;

Matches 418; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVQLVESGGDFVQPGGSLRVSQAAGFAFSAHYSAMSWRQAPGKGLMVAIISGSGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSFPMAMVRQAPGKGLMVAISTISGGRTYY 60
QY 61 SDSVAKRFTISRDNSKNTIYLQMRSLRADSAYFCTRYKLGITYYFDSWGQGLTLTVSSA 120
DB 61 RDSVAKRFTISRDNSKNTIYLQMRSLRADSAYFCTRYKLGITYYFDSWGQGLTLTVSSA 120
QY 121 STKGSPVFPPLAPSSKSTSGTAAAGCLVADYFPEPTVSMNSGALTSGVHTFPAYVQSNG 180
DB 121 STKGSPVFPPLAPSSKSTSGTAAAGCLVADYFPEPTVSMNSGALTSGVHTFPAYVQSNG 180
QY 181 LYSLSGVTVPSSSLGTQTYICNVNHPKPNNTKVKKEPKSCDKHTHCPCPAPELLGAP 240
DB 181 LYSLSGVTVPSSSLGTQTYICNVNHPKPNNTKVKKEPKSCDKHTHCPCPAPELLGAP 240
QY 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 300
DB 241 SVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 300
QY 301 TYRIVSVLTFLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
DB 301 TYRIVSVLTFLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
QY 361 TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPLVDSGSEFLYSKLTVDKSRNQ 420
DB 361 TKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPLVDSGSEFLYSKLTVDKSRNQ 420
QY 421 QGNVFSQSVMEALHNHYTQKSLSPGK 449
DB 421 QGNVFSQSVMEALHNHYTQKSLSPGK 449

Search completed: December 23, 2004, 19:35:46
Job time : 134.396 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 / Search time 31.449 Seconds

(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071
Sequence: 1 EVOLVESGDFVPGGSLRV.....IVEFLNRWTFQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1767	57.5	330	1	GHHU	IG gamma-1 chain C
2	1630.5	53.1	377	2	A23511	IG gamma-3 chain C
3	1628.5	53.0	377	2	A60764	IG gamma-3 chain C
4	1604	52.2	326	1	G2HU	IG gamma-2 chain C
5	1590.5	51.8	327	1	G4HU	IG gamma-4 chain C
6	1508.5	49.1	444	2	PC4436	monoclonal antibody
7	1487	48.4	470	2	S22080	IG heavy chain pre
8	1440.5	46.9	469	2	S37483	IG gamma-2a chain
9	1437	46.8	446	2	S40295	IG gamma-2a chain
10	1434	46.7	472	2	S31459	IG gamma-1 chain -
11	1429	46.5	374	2	S69339	IG heavy chain V r
12	1390	45.3	474	1	G2MS11	IG gamma-2b chain
13	1367.5	44.5	475	1	S01321	IG gamma-2b chain
14	1263	41.1	328	2	I47159	IG gamma-2a chain
15	1260	41.0	255	4	S31866	IG gamma-1 chain C
16	1257	40.9	328	2	I47160	IG gamma-2b chain
17	1254	40.8	234	2	PT0207	IG gamma-2b chain
18	1231	40.1	328	2	I47158	IG gamma-1 chain C
19	1230.5	40.1	323	1	GHRB	IG gamma-1 chain C
20	1227	40.0	328	2	I47161	IG gamma-3 chain C
21	1216.5	39.6	329	1	G2GP	IG gamma-2 chain C
22	1161.5	37.8	308	2	S30554	IG heavy chain C r
23	1152	37.5	326	2	PS0017	IG gamma-1 chain C
24	1151	37.5	289	1	G3HWT1	IG gamma-3 heavy c
25	1146.5	37.3	333	2	PS0018	IG gamma-2 chain C
26	1142	37.2	324	1	G1MS	IG gamma-1 chain C
27	1141	37.2	329	1	G1MSC	IG gamma-3 chain C
28	1139	37.1	393	1	G1MSM	IG gamma-1 chain C
29	1130	36.8	398	1	G3MSM	IG gamma-3 chain C

30	1126	36.7	330	1	G2MSA	IG gamma-2a chain
31	1123.5	36.6	335	1	G2MSAB	IG gamma-2a chain
32	1121	36.5	339	1	G2MSAM	IG gamma-2a chain
33	1118.5	36.4	329	2	S00847	IG gamma-2a chain
34	1112	36.2	322	2	PS0019	IG gamma-2a chain
35	1102	35.9	548	2	S38864	IG epsilon chain C
36	1092.5	35.6	327	2	S06611	IG gamma-2 chain C
37	1082	35.2	405	1	G2MSBM	IG gamma-2b chain C
38	1066	34.7	277	2	I47162	IG gamma-4 chain C
39	866.5	28.2	549	2	S04845	IG heavy chain pre
40	856.5	27.9	249	2	S69340	IG heavy chain VHI
41	820.5	26.7	241	2	S69131	IG heavy chain (DO
42	817.5	26.6	572	2	B46529	IG y heavy chain (
43	810	26.4	218	2	A36040	IG heavy chain V-I
44	792	25.8	220	2	A49444	IG gamma-1 heavy c
45	750	24.4	246	2	S38950	IG gamma chain - m

ALIGNMENTS

RESULT 1

GHHU
IG gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #next change 09-Jul-2004

C/Accession: A93433; S38861; S33887; B90563; A90564; B91668; A91723; A02146

R/Ellison, J.W.; Bereson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982

A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Accession: A93433; MUID:82274238; PMID:6287432

A/Molecule type: DNA

A/Residues: 1-330 <SLU>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers, R/Harris, L.J.

A/Note: Lys-330 is removed after translation

Submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

A/Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers, R/Harris, L.J.

A/Note: Lys-330 is removed after translation

Submitted to the EMBL Data Library, October 1992

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

A/Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers, R/Harris, L.J.

A/Note: Lys-330 is removed after translation

Submitted to the EMBL Data Library, October 1992

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

A/Note: this sequence has the Gln(17) allelic marker, 97-Lys, and the Gln(1) markers, R/Harris, L.J.

A/Note: Lys-330 is removed after translation

Submitted to the EMBL Data Library, October 1992

A/Reference number: S33887; MUID:83001943; PMID:6811139

A:Reference number: A90933; MWID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861
A/Note: the sequence was determined from the germline gene Rpink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem. J. 117, 33-47, 1970
A>Title: Human immunoglobulin subclones. Partial amino acid sequence of the constant
A:Reference number: A90249; MWID:70207560; PMID:4192639
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A/Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C:superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.8%; Score 1590.5; DB 1; Length 327;
Best Local Similarity 90.9%; Pred. No. 4,4e-82;

Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 120 ASTKGSPVPLAPSSKSTSGTALGCLVYDPEPEVTVSNMGALTSGVHTFPAYLQSS 179
DB 1 AATKGPSPVPLAPSSKSTSGTALGCLVYDPEPEVTVSNMGALTSGVHTFPAYLQSS 60
QY 180 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSDKTHTPCPAPPLDGG 239
DB 61 GLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSDKTHTPCPAPPLDGG 117
QY 240 PSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFMVYDGVENHNAKTRPEEOYN 299
DB 118 PSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFMVYDGVENHNAKTRPEEOYN 177
QY 300 STYRVVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
DB 178 STYRVVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 237
QY 360 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 419
DB 238 LTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 297
QY 420 QGQNVFSCVMHEALHNHTOKSLSLSPGK 449
DB 298 QGQNVFSCVMHEALHNHTOKSLSLSPGK 327

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: PC4436

R:Akaishi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A. Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A>Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr

A:Reference number: JCS810; MWID:98063277; PMID:9398605

A:Accession: PC4436

A:Molecule type: protein

A:Residues: 1-444 <AKA>

C/Comment: This catalytic antibody has peroxidase activity. It is directed again
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IM1>
F:122/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 49.1%; Score 1508.5; DB 2; Length 444;
Best Local Similarity 61.1%; Pred. No. 2,5e-77;

Matches 277; Conservative 73; Mismatches 90; Indels 13; Gaps 6;

QY 1 EVQLYSGGDFVQPGSLRVSCAAGFAPSHYAMSWROAPKGLFWAYIS--SGSGST 58
DB 1 EVQLYSGGDFVQPGSLRVSCAAGFAPSHYAMSWROAPKGLFWAYIS--SGSGST 60
QY 59 YSDSVKGRFTSRDNRKNTLYQKRSIARAEDSAVYFCRYVLTGYTPDSMGQTLTLTVS 118
DB 61 KYAESVGRFTSRDNRKNTLYQKRSIARAEDSAVYFCRYVLTGYTPDSMGQTLTLTVS 119
QY 119 SASYKGPSPVPLAPSSKSTSGTALGCLVYDPEPEVTVSNMGALTSGVHTFPAYLQSS 178
DB 120 SASYKGPSPVPLAPSSKSTSGTALGCLVYDPEPEVTVSNMGALTSGVHTFPAYLQSS 179
QY 179 SGLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSDKTHTPCPAPPLDGG 236
DB 180 SGLYSLSVVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVPKSDKTHTPCPAPPLDGG 234
QY 237 LGSPVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFMVYDGVENHNAKTRPEE 296
DB 235 ---SSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFMVYDGVENHNAKTRPEE 291
QY 297 QNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 356
DB 292 QNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 351
QY 357 RDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 416
DB 352 RDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 411
QY 417 SRMOQNVFSCVMHEALHNHTOKSLSLSPGK 449
DB 412 SRMOQNVFSCVMHEALHNHTOKSLSLSPGK 444

RESULT 7

S22080

Ig heavy chain precursor (B/MF.4A.17.H5.A5) - bovine

N/Altername names: Ig gamma-1 chain C region (clone 8.10)

C:Species: Bos primigenius taurus (cattle)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303

R:Sanders, P.G.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22080

A:Accession: S22080

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <SAY>

A:Cross-references: EMBL:X62916; NID:q439; PIDN:CAA44699.1; PID:q440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 1989

A>Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma

A:Reference number: S06610; MWID:90097956; PMID:5513487

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:Cross-references: EMBL:X16701

A/Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1; 111/1; 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotrimer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IM1>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 48.4%; Score 1487; DB 2; Length 470;
Best Local Similarity 62.4%; Pred. No. 4.3e-76;
Matches 284; Conservative 60; Mismatches 101; Indels 10; Gaps 6;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWROAPGKLEWVAIYSSGSGTYY 60
DB 20 QVQLRSGPGLVSKQSLTSLCTVSGFSLSYALTWRQAPGKLEWVGITISGDT-ITY 78
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRAPDSAVYFCTRVKLTGTY----YFDSMGQGLTLT 116
DB 79 NPALKSLSTIKENSKQSVLSVSSVTPEDATYTCARSTYGEVDGADADAWQGLLVT 138
QY 117 VSSASTYGPVFPPLAPSSKSTSGTALGCLVVDYFPEPVTVSNNGALTISGHTFPAVL 176
DB 139 VSSASTYAPKRYPLSSCCGDKSSSTVLGCLVSSYMEPEPVTVSNNGALTISGHTFPAVL 198
QY 177 QSSGLVSLSVVTVSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPKPAPEL 236
DB 199 QSSGLVSLSKNTVPGSTSG-QITTCNVAPHASTKVDKADP-TC-KPSPDCCPPEL 255
QY 237 LGGSPVLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREE 296
DB 256 PGGSVFIFFPKPKDTLTISGTPVTCVVVDVGHDDPEVKFQSWVDVENVATATTKREE 315
QY 297 QYNSTYRVSVLTVLHODWLNGEKYKCKVSNKALPAPIEKTISAKQPREPQVYTLPPS 356
DB 316 QFNSTYRVSVLALRIQHODWTKGKEPKCKVHNEGPAPIVRTISRTKPAPEPQVYVLA 375
QY 357 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGFPLYSKLT 414
DB 376 QEELSKSTVSLTLCWVTSFYPDYLAWEVRQNGQPESEKYGTTPPQDLADSSYFLYSKLRV 435
QY 415 DKSRMQGNVFCSCVMEALHNHYTOKSLSPK 449
DB 436 DRMSWGEGDYTCVVMHEALHNHYTOKSLSPK 470

RESULT 8
S37483
Ig gamma-2a chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37483
R/Duplicate: F.F.D.
A/Reference number: S37483
A/Accession: S37483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-469 <DUC>
A/Cross-references: EMBL:X70423; NID:G406252; PIDN:CAA9868.1; PID:G406253
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F:216-345/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 1440.5; DB 2; Length 469;
Best Local Similarity 59.1%; Pred. No. 1.7e-73;
Matches 267; Conservative 72; Mismatches 108; Indels 5; Gaps 4;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWROAPGKLEWVAIYSSGSGTYY 60
DB 20 QVQLRSGPGLVSKQSLTSLCTVSGFSLSYALTWRQAPGKLEWVGITISGDT-ITY 78
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRAPDSAVYFCTRVKLTGTY----YFDSMGQGLTLT 119
DB 80 NENKGAATLTVDTSSTATAMQSLTSSEDAVFCARAKATITLADYMGQGLTLVSS 139
QY 120 ASTGSPVFPPLAPSSKSTSGTALGCLVVDYFPEPVTVSNNGALTISGHTFPAVL 179
DB 140 AKTAPSVFPPLAPVCGDITSGSVTLGCLVKGYPPEPVTLTVNSGSLSSGHTFPAVL 199

QY 180 GLYSLSVTVTVSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCP--CPAPEL 237
DB 200 -LTLSSTVTVTVSSITNVAHPASTKYDKKIEPRG-PTIKPCPCCPAPNLL 257
QY 238 GGSVFIFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREE 297
DB 258 GGSVFIFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKPREE 317
QY 298 YNSTYRVSVLTVLHODWLNGEKYKCKVSNKALPAPIEKTISAKQPREPQVYTLPPS 357
DB 318 YNSTLRVSVLPIQHODWMSGKEPKCKVNNKDLPAPIERTISXPKGSVRAPOVYVPPPE 377
QY 358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGFPLYSKLTVDK 417
DB 378 EENYKQVTLTCVWTDPEPDITVEWNTNGKTLNKTLEPVDSDSYFMYSKLVEKK 437
QY 418 RMOGNVFCSCVMEALHNHYTOKSLSPK 449
DB 438 NWYERNYSQSVVHEGLHNHYTOKSLSPK 469

RESULT 9
S40295
Ig gamma-2a chain (mab735) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S40295
R/Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B. submitted to the EMBL Data Library, January 1993
A/Description: Primary structure of the murine monoclonal IgG2a antibody mab735 against
A/Reference number: S40295
A/Accession: S40295
A/Molecule type: protein
A/Residues: 1-446 <KLE>
A/Cross-references: UNIPROT:Q99L25
C/Genetics:
A/Map position: 12
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/disulfide bonds: #status predicted
F:132/disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/disulfide bonds: interchain #status predicted
F:257/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.8%; Score 1437; DB 2; Length 446;
Best Local Similarity 59.3%; Pred. No. 2.5e-73;
Matches 267; Conservative 70; Mismatches 107; Indels 6; Gaps 4;

QY 1 EVOLVESGDFVPGGSLRVSCAASGFAFSHYAMSWROAPGKLEWVAIYSSGSGTYY 60
DB 1 QVQLRSGPGLVSKQSLTSLCTVSGFSLSYALTWRQAPGKLEWVGITISGDT-ITY 78
QY 61 SDSVKGRFTISRDNKNTLYLQMSLRAPDSAVYFCTRVKLTGTY----YFDSMGQGLTLT 120
DB 61 NENKGAATLTVDTSSTATAMQSLTSSEDAVFCARAKATITLADYMGQGLTLVSS 138
QY 121 STGSPVFPPLAPSSKSTSGTALGCLVVDYFPEPVTVSNNGALTISGHTFPAVL 180
DB 119 KTAAPSVFPPLAPVCGDITSGSVTLGCLVKGYPPEPVTLTVNSGSLSSGHTFPAVL 177
QY 181 LYSLSVTVTVSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCP--CPAPEL 238
DB 178 LYTLSSTVTVTVSSITNVAHPASTKYDKKIEPRG-PTIKPCPCCPAPNLL 256

Db 319 THREDYNSTRIRVVALPIQHODWMSGKFKCVNNKDLPAPIERTISIKIGIVRAPOVYI 378
QY 353 LPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGCPENNYKTPPVLSDDGSFELYSKL 412
Db 379 LSPPEQLSRKQVSLTCLVAGFSPEDISYEWTSNGHTSENYKQDAPVLDSGYSFLYSKL 438
QY 413 TVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
Db 439 NMKTSKMEKTDSPSCNVRRHGLKNKYLLKKTISRSPPK 475

RESULT 14

147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A:Reference number: I47158; MID:95015845; PMID:7930579
A:Accession: I47159
A:status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <RAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetic8:
A:gene: IgG2a
C:superfamily: Immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

Query Match 41.1%; Score 1263; DB 2; Length 328;
Best local similarity 69.6%; Pred. No. 9.4e-64;

Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;

QY 120 ASTKGSPVPLADSSKSTSGTALGCLVNDYPPPEPVTVSWNSGALTSGVHTFPVAVLQSS 179
Db 1 APKTAHSVYPLAPCSRDTSQPNVALGLASSYPPPEPVTVWNSGALSSGVHTFPVAVLQSS 60
QY 180 GLYSLSSTVTVPPSSSLGTQYIICNNVHKPSNTKVDKKVBPXSCDKTHTCPCPAPBELLG 239
Db 61 GLYSLSSTVTVPPASSLSKSYTCNVNHPATTTVDKRVGKTKPCPCIPACESP---G 116
QY 240 PSYFLPPEPKQDLMISRPPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNAAKTRPEEOYN 299
Db 117 PSYFIFPPKQDLMISRPQVTCVVVDVSGENPEVQFSGYVDGVENHAAQTRPKKEQFN 176
QY 300 STYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSRDE 359
Db 177 STYRVVSVLPPIQHODWLNKKEPKCKVNNKDLPAPIRIISKAKGQTRPEPQVYTLPPHAE 236
QY 360 LITNOVSLTCLVKGFPSPDIAYEWESNGCPENNYKTPPVLSDDGSFELYSKLTVDSK 417
Db 237 LSRKVSITCLVAGFYPDIDVEMQRNGQPEPEGNYRTTPPOQVDGTYFLYSKFSVDKA 296
QY 418 RMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
Db 297 SMQGGGIFQCAVMEALHNHYTQKSLSLSPGK 328

RESULT 15

331866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A>Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products.

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>
A:Cross-references: EMBL:X70421; NID:g333068; PIDN:CAA49866.1; PID:g333069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 41.0%; Score 1260; DB 4; Length 255;
Best local similarity 97.5%; Pred. No. 1e-63;

Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 211 TVDKKXVEPKSCDKTHTCPCPAPBELGSPSFLPPEPKQDLMISRPPEVTCVVVDVSH 270
Db 17 TVAQADVSKSCDKTHTCPCPAPBELGSPSVFLPPEPKQDLMISRPPEVTCVVVDVSH 76
QY 271 EDPEVKFNNYVDSGEVHNAAKTRPEEOYNSTRVSVLTVTHQDMLNGKEYCKVSNKAL 330
Db 77 EDPEVKFNNYVDSGEVHNAAKTRPEEOYNSTRVSVLTVTHQDMLNGKEYCKVSNKAL 136
QY 331 PAPIEKTSKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGQPE 390
Db 137 PAPIEKTSKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGQPE 196
QY 391 NNYKTPPVLSDDGSFELYSKLTVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
Db 197 NNYKTPPVLSDDGSFELYSKLTVDSKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 255

Search completed: December 23, 2004, 19:06:04

Job time : 33.449 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 161.904 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-53

Perfect score: 3071

Sequence: 1 EVOLVBSGGDFVPGGSLRV.....IVEFLNRWTFQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0, Gapect 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2226.5	72.5	471	2 AAH24289	Aah24289 homo sapi
2	2223	72.4	470	2 O6RJA4	O6RJA4 homo sapien
3	2223	72.4	470	2 AAH18747	Aah18747 homo sapi
4	2212	72.0	478	2 O6PI81	O6PI81 homo sapien
5	2212	72.0	478	2 AAH41037	Aah41037 homo sapi
6	2211.5	72.0	475	2 O6MZ06	O6MZ06 homo sapien
7	2211.5	72.0	475	2 CAE45972	Ca45972 homo sapi
8	2191.5	71.4	473	2 O6MZV7	O6MZV7 homo sapien
9	2191.5	71.4	473	2 CAE45920	Ca45920 homo sapi
10	2191	71.3	472	2 BAC85232	Bac85232 homo sapi
11	2188.5	71.3	475	2 O6GMW7	O6GMW7 homo sapien
12	2187	71.2	466	2 O6IN78	O6IN78 homo sapien
13	2187	71.2	472	2 O6N089	O6N089 homo sapien
14	2187	71.2	472	2 CAE45781	Ca45781 homo sapi
15	2185.5	71.2	479	2 AAH06402	Aah06402 homo sapi
16	2184.5	71.1	544	2 O6PJ95	O6PJ95 homo sapien
17	2184.5	71.1	544	2 AAH19046	Aah19046 homo sapi
18	2173	70.8	468	2 BAC85444	Bac85444 homo sapi
19	2172	70.7	480	2 O6N094	O6N094 homo sapien
20	2172	70.7	480	2 CAE45776	Ca45776 homo sapi
21	2159	70.3	466	2 O6N096	O6N096 homo sapien
22	2159	70.3	466	2 CAE45774	Ca45774 homo sapi
23	2158	70.3	470	2 Q725W1	Q725W1 homo sapien
24	2149.5	70.0	473	2 O6P055	O6P055 homo sapien
25	2149.5	70.0	473	2 AAH65820	Aah65820 homo sapi
26	2147.5	69.9	471	2 BAC85388	Bac85388 homo sapi
27	2145	69.8	470	2 BAC85172	Bac85172 homo sapi
28	2144	69.8	466	2 AAH64496	Aah64496 homo sapi
29	2142	69.7	478	2 BAC85385	Bac85385 homo sapi
30	2136	69.6	464	2 BAC85373	Bac85373 homo sapi
31	2134	69.5	482	2 Q72351	Q72351 homo sapien

32	2123	69.1	474	2 BAC85350	Bac85350 homo sapi
33	2113.5	68.8	479	2 AAH14667	Aah14667 homo sapi
34	2109	68.7	464	2 AAH19337	Aah19337 homo sapi
35	2107	68.6	468	2 BAC85175	Bac85175 homo sapi
36	2105.5	68.6	481	2 O6N097	O6N097 homo sapien
37	2105.5	68.6	481	2 CAE45773	Ca45773 homo sapi
38	2096	68.3	474	2 BAC85171	Bac85171 homo sapi
39	2084	67.9	472	2 BAC86225	Bac86225 homo sapi
40	2083.5	67.8	469	2 Q727P5	Q727P5 homo sapien
41	2082	67.8	470	2 AAH62336	Aah62336 homo sapi
42	2076	67.6	476	2 BAC05017	Bac05017 homo sapi
43	2075	67.6	478	2 BAC86514	Bac86514 homo sapi
44	2070	67.4	474	2 BAC05012	Bac05012 homo sapi
45	2069.5	67.4	473	2 BAC05013	Bac05013 homo sapi

ALIGNMENTS

RESULT 1	ID	AAH24289	PRELIMINARY;	PRT;	471 AA.
AC	AAH24289;				
DT	02-MAR-2004 (TEMBLrel. 27, Created)				
DT	02-MAR-2004 (TEMBLrel. 27, Last sequence update)				
DT	02-MAR-2004 (TEMBLrel. 27, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Sp1en;				
RX	MDLLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,				
RA	Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,				
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				
RA	Boeak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huix S.W.,				
RA	Vallalou D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,				
RA	Jones S.J., Matra M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Sp1en;				
RA	Strausberg R.,				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: BC024289; AAH24289.1; -				
KW	Hypothetical protein.				
SQ	SEQUENCE 471 AA; 51791 MW; 38877P4CF588660E CRC64;				
Query Match 72.5%; Score 2226.5; DB 2; Length 471;					
Best Local Similarity 92.9%; Pred. No. 7,7e-137;					
Matches 420; Conservative 15; Mismatches 14; Indels 3; Gaps 2;					
QY	1 EVOLVBSGGDFVPGGSLRVCAAGPAPSHVMSVROAPGKGLWAVAYISGSGGTY 60				
DB	20 EVOLVBSGGDFVPGGSLRVCAAGPAPSHVMSVROAPGKGLWAVAYISGSGGTY 79				
QY	61 SDSVKKRFTISRNSKNTLYLQWRSLRADBSANVYFCTR--VTKGTY-YFDSWGQGLTV 117				

Db	80	ADSVAGRFITSDNNAKNSLYLOMNSIRAEEDTAVYTCARDIRQLTSTWYFDLMGRGILVY	139
Qy	118	SSASTKGPSVFPFLAPSSKSTSGGTAAAGCLVYDYPEPYTVSNMNGALTSVGTFFPAVLQ	177
Db	140	SSASTKGPSVFPFLAPSSKSTSGGTAAAGCLVYDYPEPYTVSNMNGALTSVGTFFPAVLQ	199
Qy	178	SSGLTSLSSVTVVPSSSLGTQYIICVMNHNKPSNTKYDKDKVEPSCPKTHGPCPCPAPELL	237
Db	200	SSGLTSLSSVTVVPSSSLGTQYIICVMNHNKPSNTKYDKDKVEPSCPKTHGPCPCPAPELL	259
Qy	238	GGPSVFLPFPKPKDXTLMIISRTPEVTCVVVDVSHEDDEVKNMYVDGVENAAATKPREEQ	297
Db	260	GGPSVFLPFPKPKDXTLMIISRTPEVTCVVVDVSHEDDEVKNMYVDGVENAAATKPREEQ	319
Qy	298	YNSTRYRVSVTVLVLMODMWNGKEVKCCKVSNKALPAPIEKTISAKAKOPREPOVYTLPPSR	357
Db	320	YNSTRYRVSVTVLVLMODMWNGKEVKCCKVSNKALPAPIEKTISAKAKOPREPOVYTLPPSR	379
Qy	358	DELTAQNQSVLTCLVNGFYPSDILAVEMESNGQPENNKTTTPVLDSDSGSFFLYSKLTIVDKS	417
Db	380	DELTAQNQSVLTCLVNGFYPSDILAVEMESNGQPENNKTTTPVLDSDSGSFFLYSKLTIVDKS	439
Qy	418	RMQOGNVSCSVNHEALNNHTYQKSLSLSPBK	449
Db	440	RMQOGNVSCSVNHEALNNHTYQKSLSLSPBK	471

RESULT 2			
Q6PJ04	PRELIMINARY;	PRT;	470 AA.
ID	Q6PJ04		
AC	Q6PJ04;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RX	MEDLINE=22386257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditschenko L., Marzina K., Farmer A.S., Rubin G.M., Hong L.,		
RA	Stepston M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ueffing T.B., Tohyama S., Carninci P., Frange C.,		
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywninski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
RA	Strausberg R.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBD databases.		
DR	EMBL, BC018747, AA018747.1; -		
DR	InterPro: IPR003599; IG.		
DR	InterPro: IPR007110; IG-like.		
DR	InterPro: IPR003597; IG cl.		

DR InterPro; IPR003306; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11ED7D99 CRC64;

Query Match	72.4%	Score 2223	DB 23	Length 470
Best Local Similarity	93.1%	Pred. No. 1.3e-136		
Matched 420	Conservative 7	Mismatches 22	Indels 2	Gaps 1
QY	1	EVOLVESGGDVFVQPGSGLRVSCAASGAFASHYAMSWVRQAPGKGLBMWAYISSGSGSTYY	60	
DB	20	EVOLVESGGGLVQPGSGLRSLSCVWSGPFSSXWMSWVRQAPGKGLBMWANIKODGSEKKY	79	
QY	61	SDSVKGRFTISRDNKSNKFLYQMSLRBEDSAVYVCTEVLKGTYY--YFDSWQGGILLTYS	118	
DB	80	VDSVKGRFTISRDNKSNKFLYQMSLRBEDTAIVYCAADGSSWYDWFDPWQGGILLTVS	139	
QY	119	SASTKGPEVFPFLAPSSKSTSGTALGCLVNDYFPEPYTVSNWGALTSVHTPRAVLQS	178	
DB	140	SASTKGPEVFPFLAPSSKSTSGTALGCLVNDYFPEPYTVSNWGALTSVHTPRAVLQS	199	
QY	179	SGLYSLSSVTVVPSSSLGTQTYICVNHKPSNTKYDKKVEPSSCKHTTCCPCAPABELG	238	
DB	200	SGLYSLSSVTVVPSSSLGTQTYICVNHKPSNTKYDKKVEPSSCKHTTCCPCAPABELG	259	
QY	239	GPSVFLFPPEKPDLTMSRTEPEVTCVVVDVSHEDPEVFNNYVDGVEYHNAATKRCREBOY	298	
DB	260	GPSVFLFPPEKPDLTMSRTEPEVTCVVVDVSHEDPEVFNNYVDGVEYHNAATKRCREBOY	319	
QY	299	NSTRVNVSVTLVHODMLNGKEYKCKVSNKALPAIEKTIISAKQKQPREPQYTLIPPSND	358	
DB	320	NSTRVNVSVTLVHODMLNGKEYKCKVSNKALPAIEKTIISAKQKQPREPQYTLIPPSND	379	
QY	359	ELTKNQVSLTCLVKGFPSPDIAVWESNGOPENNKTTTPVLDSDGSFELYSKLTVDKSR	418	
DB	380	ELTKNQVSLTCLVKGFPSPDIAVWESNGOPENNKTTTPVLDSDGSFELYSKLTVDKSR	439	
QY	419	WQGNVPSGCSWHEALHNHYTQKSLSLSPGK	449	
DB	440	WQGNVPSGCSWHEALHNHYTQKSLSLSPGK	470	

RESULT 3			
AAH18747			
ID	AAH18747	PRELIMINARY;	PRT; 470 AA.
AC	AAH18747;		
DT	02-MAR-2004 (TREMBLrel. 27, Created)		
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)		
DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Primary B-Cells;		
FX	MEDLINE=22388257; PubMed=12477932;		
RA	Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Ditcheenko L., Marinisa K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Cacaavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Yoshiyuki S., Carninci P., Prange C.,		
RA	Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
KM Hypothetical protein.
SO SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 72.4%; Score 2223; DB 2; Length 470;
Best Local Similarity 93.1%; Pred. No. 1.3e-136;
Matches 420; Conservative 7; Mismatches 22; Indels 2; Gaps 1;

QY 1 EVOLVESGDFVPGSGSLRVSCAASGFARSHYMSWVRQAPGKGLEWVAIYSSGSGSTYY 60
DB 20 EVOLVESGGLVPGGSLRLSCVSGFTSSYMSWVRQAPGKGLEWVAIYKODGSEKYY 79
QY 61 SDSVKGRTTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTY--VFDSMGQGLTLTVS 118
DB 80 VDSVKGRTTISRDNKNTLYLQNRSLRAEDTAIYVCARDSSWYRDMFDKGGGTLTVS 139
QY 119 SASSTKGPVPLAPSSKSTSGGTALGCLVYDYPPEPVTVSWSGALTSGVHTFPAVLQS 178
DB 140 SASSTKGPVPLAPSSKSTSGGTALGCLVYDYPPEPVTVSWSGALTSGVHTFPAVLQS 199
QY 179 SGILYSLSSVTVTPSSSLGTQTYICNVNKKPSNTVDKKVPEKSCDKHTHPCGAPRLG 238
DB 200 SGILYSLSSVTVTPSSSLGTQTYICNVNKKPSNTVDKKVPEKSCDKHTHPCGAPRLG 259
QY 239 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAKTPREOY 298
DB 260 GPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAKTPREOY 319
QY 299 NSTYRVVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 358
DB 320 NSTYRVVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 379
QY 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 418
DB 380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
QY 419 MOQGNVFSGVMEHAIHNYTOKSLSPK 449
DB 440 MOQGNVFSGVMEHAIHNYTOKSLSPK 470

RESULT 4
06P181
ID 06P181 PRELIMINARY; PRT; 478 AA.
AC 06P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TI Tissue=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Pelting E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsugu S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyanski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-11ke.
DR InterPro; IPR003597; IG-1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sec; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SO SEQUENCE 478 AA; 52666 MW; 17BED38D91970D6 CRC64;

Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 6.9e-136;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;

QY 1 EVOLVESGDFVPGSGSLRVSCAASGFARSHYMSWVRQAPGKGLEWVAIYSSGSGSTYY 60
DB 20 EVOLVESGGLVPGGSLRLSCVSGFTSSYMSWVRQAPGKGLEWVAIYKODGSEKYY 79
QY 61 SDSVKGRTTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLGTYF--DSWG 110
DB 80 VDSVKGRTTISRDNKNTLYLQNRSLRAEDTAIYVCAREESTMTVNAIYFYFVDVWG 139
QY 111 QGTLTVSSASTGSPVPLAPSSKSTSGGTALGCLVYDYPPEPVTVSWSGALTSGVH 170
DB 140 KGTITVSSASTGSPVPLAPSSKSTSGGTALGCLVYDYPPEPVTVSWSGALTSGVH 199
QY 171 TFPVAVQSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTVDKKVPEKSCDKHTHPCP 230
DB 200 TFPVAVQSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTVDKKVPEKSCDKHTHPCP 259
QY 231 CPAPRLGSPVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAK 290
DB 260 CPAPRLGSPVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAK 319
QY 291 TKREQVNSTYRVVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPOV 350
DB 320 TKREQVNSTYRVVSVLTVLHODWLNKGEYKCVSNKALPAPIEKTISKAKGQPREPOV 379
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 410
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS 439

```
QY 411 KLTVDKSRWQGGNVFSCSYMHGALHNHYTQKSLSPGK 449
Db 440 KLTVDKSRWQGGNVFSCSYMHGALHNHYTQKSLSPGK 478

RESULT 5
AAH41037 PRELIMINARY; PRT; 478 AA.
ID AAH41037
AC AAH41037
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.,
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBU; BC041037; AAH41037.1; -.
RW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;
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Query Match 72.0%; Score 2212; DB 2; Length 478;
Best Local Similarity 91.3%; Pred. No. 6.9e-136;
Matches 419; Conservative 10; Mismatches 20; Indels 10; Gaps 2;
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QY 1 EVOLVSSGGDFVOPGGSRLRVSCAASGPAFSGHYAMSVWRAPGKGLMVAIVYISSGSGSTY 60
Db 20 EVOLVSSGGGLVOPGGSRLRVSCAASGFTTSSYMSVWRAPGKGLMVAIVYISSGSEKTY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTR-----VKLGTYTF--DSWG 110
Db 80 VDSVKGRTTISRDNKNTLYLQMRSLRAEDTAVYCARPESTMTTVNADYFFVWDVWG 139
QY 111 OGTLTVSSASTGSGVFPPLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNAGALTSGVHTP 170
Db 140 KGTTVVSSASTGSGVFPPLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNAGALTSGVHTP 199
QY 171 TTPAVVQSSGLVSSVTVVPPSSLGTOITYICNVNHPKSTKYDKKVEPKSCDKHTCP 230
Db 200 TTPAVVQSSGLVSSVTVVPPSSLGTOITYICNVNHPKSTKYDKKVEPKSCDKHTCP 259
QY 231 CPABELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAK 290
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Db 260 CPABELLGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAK 319
QY 291 TKPREQVNSTYRVSVTLTVLHODMUNGKEYCKVSNKALPAPIEKTISKAKGPREPOV 350
Db 320 TKPREQVNSTYRVSVTLTVLHODMUNGKEYCKVSNKALPAPIEKTISKAKGPREPOV 379
QY 351 YTLPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGQENNYKTPPYLDSDGSFFLYS 410
Db 380 YTLPPSRDEMTNQVSLTCLVGFYPSDIAVWESNGQENNYKTPPYLDSDGSFFLYS 439
QY 411 KLTVDKSRWQGGNVFSCSYMHGALHNHYTQKSLSPGK 449
Db 440 KLTVDKSRWQGGNVFSCSYMHGALHNHYTQKSLSPGK 478
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```
RESULT 6
Q6MZ06 PRELIMINARY; PRT; 475 AA.
ID Q6MZ06
AC Q6MZ06;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Oesanger A., Fobo G.,
RA Han M., Wilmann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RW EMBU; BX640947; CAE45972.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-secl; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
RW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE25A26F4B8E CRC64;
```

```
Query Match 72.0%; Score 2211.5; DB 2; Length 475;
Best Local Similarity 91.2%; Pred. No. 7.4e-136;
Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;
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QY 1 EVOLVSSGGDFVOPGGSRLRVSCAASGPAFSGHYAMSVWRAPGKGLMVAIVYISSGSGSTY 60
Db 20 EVOLVSSGGGLVOPGGSRLRVSCAASGFTTSSYMSVWRAPGKGLMVAIVYISSGSEKTY 79
QY 61 SDSVKGRTTISRDNKNTLYLQMRSLRAEDSAVYFCTR-----YFDSWQGT 113
Db 80 ADSVKGRTTISRDNKNTLYLQMRSLRADDTAVYCARADYNDYQVAPYVYFDVWGRGT 139
QY 114 LITVSSASTGSGVFPPLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNAGALTSGVHTP 173
Db 140 LVSVAASASTGSGVFPPLAPSSKSTSGGTAALGCLVXDYPPEVTVVSNAGALTSGVHTP 199
QY 174 AVVQSSGLVSSVTVVPPSSLGTOITYICNVNHPKSTKYDKKVEPKSCDKHTCP 233
Db 200 AVVQSSGLVSSVTVVPPSSLGTOITYICNVNHPKSTKYDKKVEPKSCDKHTCP 259
QY 234 PELVGGPSVFLPPEPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAK 293
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Db 260 PELLGSPVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 319

Qy 294 REEQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 353

Db 320 REEQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 379

Qy 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 413

Db 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 439

Qy 414 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 440 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 7

CAE45972 PRELIMINARY; PRT; 475 AA.

AC CAE45972;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686G1190.

GN DKFZp686G1190.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;

RA Lauber J., Bahr A., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,

RA Han M., Wiemann S.;

RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640947; CAE45972.1; -.

KM Hypothetical protein.

SO SEQUENCE 475 AA; 52043 MW; B7EAE25A26F48BE CRC64; .

Query Match 72.0%; Score 2211.5; DB 2; Length 475;

Best Local Similarity 91.2%; Pred. No. 7.4e-136;

Matches 416; Conservative 13; Mismatches 20; Indels 7; Gaps 1;

Qy 1 EVOLVSGGDFVQPGSLRVSCAAGFAFSHYAMSVWRAPGKGLMVAIYSSGSGTTY 60

Db 20 EVOLVSGGGLVQPGSLRVSCAAGFTFSFEMNVWRAPGKGLMVAIYSSGSGTTY 79

Qy 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLTGY-----YFDSWGQGT 113

Db 80 ADSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLTGY-----YFDSWGQGT 139

Qy 114 LTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173

Db 140 LTVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy 174 AVLOSGLVLSVSVTVVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPCPAP 233

Db 200 AVLOSGLVLSVSVTVVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPCPAP 259

Qy 234 PELLGSPVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 293

Db 260 PELLGSPVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 319

Qy 294 REEQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 353

Db 320 REEQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 379

Qy 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 413

Db 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 439

Qy 414 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 440 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 8

Q6MZV7 PRELIMINARY; PRT; 473 AA.

AC Q6MZV7;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686C11235.

GN Name=DKFZp686C11235;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human small intestine;

RG THE GERMAN HUMAN CDNA CONSORTIUM;

RA Bioecker H., Bioecker M., Mewes H.W., Well B., Amid C., Osanger A.,

RA Fobo G., Han M., Wiemann S.;

RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640853; Q6MZV7.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR003599; IG-1ike.

DR InterPro; IPR003597; IG-1.

DR InterPro; IPR003596; IG-1.

DR Pfam; PF00047; IG-1.

DR SMART; SM00409; IG-1.

DR SMART; SM00409; IG-1.

DR SMART; SM00406; IG-1.

DR PROSITE; PS00835; IG-1.

DR PROSITE; PS00290; IG-1.

KM Hypothetical protein.

SO SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64; .

Query Match 71.4%; Score 2191.5; DB 2; Length 473;

Best Local Similarity 90.1%; Pred. No. 1.5e-134;

Matches 409; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

Qy 1 EVOLVSGGDFVQPGSLRVSCAAGFAFSHYAMSVWRAPGKGLMVAIYSSGSGTTY 60

Db 20 EVOLVSGGGLVQPGSLRVSCAAGFTFSFEMNVWRAPGKGLMVAIYSSGSGTTY 79

Qy 61 SDSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLTGY-----YFDSWGQGT 113

Db 80 ADSVKGRFTISRDNKNTLYLQNRSLRAEDSAVYFCTRVKLTGY-----YFDSWGQGT 139

Qy 116 TVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 175

Db 140 TVSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 199

Qy 176 LOSGGLVLSVSVTVVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPCPAP 235

Db 200 LOSGGLVLSVSVTVVSSSLGTQTYICNVNHPKSNKVDKVEPKSCDTHTCPCPAP 259

Qy 236 LILGSPVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 295

Db 260 LILGSPVFLFPKPKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAKTKP 319

Qy 296 EQQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 355

Db 320 EQQYNTRYVSVLTVLHODMLNGKEYKCKVSKALPAPIEKTISKAKGPREPOVYTL 379

Qy 356 SPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 415

Db 380 SPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQPENNYKTPPVLDSDGSFFLYSKLT 439

Qy 416 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 440 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 473

RESULT 9
CAE45920 PRELIMINARY; PRT; 473 AA.
AC CAE45920;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN DKFZp686C11235.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloeker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BF6447 CRC64;

Query Match 71.4%; Score 2191.5; DB 2; Length 473;
Best Local Similarity 90.1%; Pred. No. 1.5e-134;
Matches 409; Conservative 21; Mismatches 19; Indels 5; Gaps 1;

QY 1 EVQLVDSGGDFVQPGSLRVSCAAGFAFSHYAMSWRQAPGKGLWVAIYSSGSGITY 60
DB 20 EIVNLQSGGGLVQPGSLRLSCAAGFAFGGTAMTWVRQVPGKGLWVAISGSGITY 79
QY 61 SDSVKGRFTISRDNSKNTLYIQMNSLRADSAVYECTRYKLGTY-----YFDSWGGTLL 115
DB 80 ADSLVKGRFTISRDNSKNTLYIQMNSLRADSAVYECTRYKLGTY-----YFDSWGGTLL 139
QY 116 TVSSASTKGPVFPPLAPSSKSTSGGTAAGCLVDFPEPVTVSMNSGALTSGVHTFPA 175
DB 140 TVSSASTKGPVFPPLAPSSKSTSGGTAAGCLVDFPEPVTVSMNSGALTSGVHTFPA 199
QY 176 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHRKPSNTVDKKEVPSKCDKTHTCPCPAP 235
DB 200 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHRKPSNTVDKKEVPSKCDKTHTCPCPAP 259
QY 236 LIGGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEKFNWYDGVENNAKTKPR 295
DB 260 LIGGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEKFNWYDGVENNAKTKPR 319
QY 296 EGYNSTYRVVSVLVTLVHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 355
DB 320 EGYNSTYRVVSVLVTLVHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 379
QY 356 SRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 415
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 439
QY 416 KSRWQOGNVFSCSYMHEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQOGNVFSCSYMHEALHNHYTQKSLSLSPGK 473

RESULT 10
BAC85232 PRELIMINARY; PRT; 472 AA.
AC BAC85232;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ26265 fig. clone DMC05516, highly similar to Ig gamma-1 chain C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=dermoid tumor;
RA Hata H., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK129776; BAC85232.1; -.
SQ SEQUENCE 472 AA; 51212 MW; 01BPF215F9809164 CRC64;

Query Match 71.3%; Score 2191; DB 2; Length 472;
Best Local Similarity 90.1%; Pred. No. 1.6e-134;
Matches 410; Conservative 17; Mismatches 20; Indels 8; Gaps 2;

QY 1 EVQLVDSGGDFVQPGSLRVSCAAGFAFSHYAMSWRQAPGKGLWVAIYSSGSGITY 60
DB 20 EIVNLQSGGGLVQPGSLRLSCAAGFAFGGTAMTWVRQVPGKGLWVAISGSGITY 79
QY 61 SDSVKGRFTISRDNSKNTLYIQMNSLRADSAVYECTRYKLGTY-----YFDSWGGTLL 114
DB 80 ADSLVKGRFTISRDNSKNTLYIQMNSLRADSAVYECTRYKLGTY-----YFDSWGGTLL 137
QY 115 LTVSSASTKGPVFPPLAPSSKSTSGGTAAGCLVDFPEPVTVSMNSGALTSGVHTFPA 174
DB 138 LTVSSASTKGPVFPPLAPSSKSTSGGTAAGCLVDFPEPVTVSMNSGALTSGVHTFPA 197
QY 175 VLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHRKPSNTVDKKEVPSKCDKTHTCPCPAP 234
DB 198 VLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHRKPSNTVDKKEVPSKCDKTHTCPCPAP 257
QY 235 ELIGGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEKFNWYDGVENNAKTKPR 294
DB 258 ELIGGSPVFLPPPKKDTLMIISRTPEVTCVVDVSHEDPEKFNWYDGVENNAKTKPR 317
QY 295 EGYNSTYRVVSVLVTLVHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 354
DB 318 EGYNSTYRVVSVLVTLVHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPP 377
QY 355 PSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 414
DB 378 PSRDELTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 437
QY 415 DKSRWQOGNVFSCSYMHEALHNHYTQKSLSLSPGK 449
DB 438 DKSRWQOGNVFSCSYMHEALHNHYTQKSLSLSPGK 472

RESULT 11
Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Nak S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Uedlin T.B., Tooshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RC Strausberg R.;
 RL EMBL: BC073782; AAH73782.1; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00647; Ig-set; 3.
 DR Pfam: PF00647; Ig; 4.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00406; IG1; 1.
 DR PROSITE: PSS0835; IG_MHC; 4.
 DR PROSITE: PSS00290; IG_LIKE; 4.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;

Query Match 71.3%; Score 2188.5; DB 2; Length 475;
 Best Local Similarity 91.0%; Pred. No. 2,3e-134;
 Matches 415; Conservative 11; Mismatches 23; Indels 7; Gaps 2;

QY 1 EVOLVESGDFVOPGGSLVSCAAGFAFSHYAMSVWRAPGKGLWVAIYSSGSGTYY 60
 DB 20 EVOLVESGGGLVOPGGSLVSCAAGFAFSHYAMSVWRAPGKGLWVAIYSSGSGTYY 79
 QY 61 SDVSKRFTISRNSKNTLYLQNRSLAEDSAVYFCFTRVK-----LGTYY-EDSWGQT 113
 DB 80 ADSVKRFTISRNSKNTLYLQNRSLAEDSAVYFCFTRVK-----LGTYY-EDSWGQT 139
 QY 114 LTVSSASATGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPVTVSNVSGALTSGVHTFP 173
 DB 140 TVVSSASATGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPVTVSNVSGALTSGVHTFP 199
 QY 174 AVLOSSGLVSLSSVTVPSSSLGTQYICNVNHPSTNTKVDKVEPKSCDKHTCPPCA 233
 DB 200 AVLOSSGLVSLSSVTVPSSSLGTQYICNVNHPSTNTKVDKVEPKSCDKHTCPPCA 259
 QY 234 PELLGSPVFLPFPKPKDTLMISRTPEVTCVVDVSHEDDEPKVKNVYDGVENNAKTKP 293
 DB 260 PELLGSPVFLPFPKPKDTLMISRTPEVTCVVDVSHEDDEPKVKNVYDGVENNAKTKP 319
 QY 294 REEYNSVTVSVVLTATLHODMLNGKYEKKCKVSNKALPAIEKTIISAKGQPREPOVYTL 353
 DB 320 REEYNSVTVSVVLTATLHODMLNGKYEKKCKVSNKALPAIEKTIISAKGQPREPOVYTL 379
 QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 413
 DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 439
 QY 414 VDKSRNQOGNVFSCSVNHEALNHNHYTOKSLISLSPGK 449
 DB 440 VDKSRNQOGNVFSCSVNHEALNHNHYTOKSLISLSPGK 475

RESULT 12

06IN78
 ID 06IN78 PRELIMINARY; PRT; 466 AA.
 AC 06IN78;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,
 RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Tooshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RC Strausberg R.;
 RL EMBL: BC072419; AAH72419.1; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00647; Ig-set; 3.
 DR Pfam: PF00647; Ig; 4.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00407; IG1; 3.
 DR SMART: SM00406; IG1; 1.
 DR PROSITE: PSS0835; IG_MHC; 4.
 DR PROSITE: PSS00290; IG_LIKE; 4.
 KW Hypothetical protein.
 SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCBDB1076E CRC64;

Query Match 71.2%; Score 2187; DB 2; Length 466;
 Best Local Similarity 92.0%; Pred. No. 2,9e-134;
 Matches 415; Conservative 11; Mismatches 19; Indels 6; Gaps 3;

QY 1 EVOLVESGDFVOPGGSLVSCAAGFAFSHYAMSVWRAPGKGLWVAIYSSGSGTYY 60
 DB 20 EVOLVESGGGLVOPGGSLVSCAAGFAFSHYAMSVWRAPGKGLWVAIYSSGSGTYY 78
 QY 61 SDVSKRFTISRNSKNTLYLQNRSLAEDSAVYFCFTRVKLTYYEDS--WGQSTLLTVS 118
 DB 79 ADSVKRFTISRNSKNTLYLQNRSLAEDSAVYFCFTRVKLTYYEDS--WGQSTLLTVS 135
 QY 119 SASATGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPVTVSNVSGALTSGVHTFPVLOS 178
 DB 136 SASATGSPVFLPAPSSKSTSGGTALGCLVKDYFPEPVTVSNVSGALTSGVHTFPVLOS 195
 QY 179 SGLYSLSSVTVPSSSLGTQYICNVNHPSTNTKVDKVEPKSCDKHTCPPEAPELLG 238

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DB 196 SGLYSLSSVTVTPSSSLGTYIICNVNHPSTNTKVDKRVKSPKCDKTHCPCPAPBELLG 255
QY 239 GSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTREEDY 298
DB 256 GSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTREEDY 315
QY 299 NSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPPSD 358
DB 316 NSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPPSD 375
QY 359 ELTKQVSLTCLVKGFYPSPDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTIVDKR 418
DB 376 ELTKQVSLTCLVKGFYPSPDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTIVDKR 435
QY 419 MOGQNVFSCSVNHEALHNHYTOKSLSLSPGK 449
DB 436 MOGQNVFSCSVNHEALHNHYTOKSLSLSPGK 466
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RESULT 13

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ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666p15220.
GN Name=DKFZp666p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Wambuit R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
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Query Match 71.2%; Score 2187; DB 2; Length 472;

Best Local Similarity 91.2%; Pred. No. 2.9e-134; Matches 414; Conservative 13; Mismatches 21; Indels 6; Gaps 3;

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QY 1 EVQLVESGGDIFYQPGSLRVSQAAGFAFSHYAMSVNRQAPGKGLEWVAIISGSGSTYY 60
DB 20 EVQLVESGGGLVQPGSRRLRSCAAGFTFDYAMHWVRQAPGKGLEWVGISWNGSILAY 79
QY 61 SSVYGRFTISRDNSKNTLYLQMRSLLRAEDSAVYFCTRVKLT--YF--DSWGQTL 115
DB 80 ADSVYGRFTISRDNSKNTLYLQMRSLLRAEDTALYYCAK-EIGAHNFTYYGMDVMWGQGTIV 138
QY 116 TVSSASTGKPSVFLPAPSSKTSGGTALAGCLVQDFPEPVTYVSNNGALTSGVHTFPAY 175
DB 139 TVSSASTGKPSVFLPAPSSKTSGGTALAGCLVQDFPEPVTYVSNNGALTSGVHTFPAY 198
QY 176 LQSSGLYSLSSVTVTPSSSLGTYIICNVNHPSTNTKVDKRVKSPKCDKTHCPCPAPE 235
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DB 199 LQSSGLYSLSSVTVTPSSSLGTYIICNVNHPSTNTKVDKRVKSPKCDKTHCPCPAPE 258
QY 236 LLGGSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTRE 295
DB 259 LLGGSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTRE 318
QY 296 EGYNSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPP 355
DB 319 EGYNSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPP 378
QY 356 SRDELTKQVSLTCLVKGFYPSPDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTIVD 415
DB 379 SRDELTKQVSLTCLVKGFYPSPDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTIVD 438
QY 416 KSRMOGQNVFSCSVNHEALHNHYTOKSLSLSPGK 449
DB 439 KSRMOGQNVFSCSVNHEALHNHYTOKSLSLSPGK 472
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RESULT 14

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ID CAB45781 PRELIMINARY; PRT; 472 AA.
AC CAB45781;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp666p15220.
GN Name=DKFZp666p15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Wambuit R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
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Query Match 71.2%; Score 2187; DB 2; Length 472;

Best Local Similarity 91.2%; Pred. No. 2.9e-134; Matches 414; Conservative 13; Mismatches 21; Indels 6; Gaps 3;

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QY 1 EVQLVESGGDIFYQPGSLRVSQAAGFAFSHYAMSVNRQAPGKGLEWVAIISGSGSTYY 60
DB 20 EVQLVESGGGLVQPGSRRLRSCAAGFTFDYAMHWVRQAPGKGLEWVGISWNGSILAY 79
QY 61 SSVYGRFTISRDNSKNTLYLQMRSLLRAEDSAVYFCTRVKLT--YF--DSWGQTL 115
DB 80 ADSVYGRFTISRDNSKNTLYLQMRSLLRAEDTALYYCAK-EIGAHNFTYYGMDVMWGQGTIV 138
QY 116 TVSSASTGKPSVFLPAPSSKTSGGTALAGCLVQDFPEPVTYVSNNGALTSGVHTFPAY 175
DB 139 TVSSASTGKPSVFLPAPSSKTSGGTALAGCLVQDFPEPVTYVSNNGALTSGVHTFPAY 198
QY 176 LQSSGLYSLSSVTVTPSSSLGTYIICNVNHPSTNTKVDKRVKSPKCDKTHCPCPAPE 235
DB 199 LQSSGLYSLSSVTVTPSSSLGTYIICNVNHPSTNTKVDKRVKSPKCDKTHCPCPAPE 258
QY 236 LLGGSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTRE 295
DB 259 LLGGSVFLFPKPKDPTLMISTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKTRE 318
QY 296 EGYNSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPP 355
DB 319 EGYNSTYRVVSVLTITLHODMNLGKEYCKVSNKALPAPIEKTISAKAQPREPOVYITLPP 378
QY 356 SRDELTKQVSLTCLVKGFYPSPDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTIVD 415
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Dh 379 SRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYYKTPPTVLDSGSPFLYKSLTVD 438
Qy 416 KSRWQGNVSPSCSYMEALNNHYTKSLSPGK 449
Db 439 KSRWQGNVSPSCSYMEALNNHYTKSLSPGK 472

RESULT 15

AAH06402
ID AAH06402 PRELIMINARY; PRT; 479 AA.
AC AAH06402;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cell;
RC MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cell;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006402; AAH06402.1; -.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 52281 MW; D74E0C98082A9788 CRC64;

Query Match 71.2%; Score 2185.5; D8 2; Length 479;
Best Local Similarity 90.0%; Pred. No. 3,7e-134;
Matches 414; Conservative 13; Mismatches 22; Indels 11; Gaps 2;

Qy 1 EVOLVESGDFVOPGSLRVSCAAGFASHYAMSVTRQAPGKLEWVAVISSGSGSTYY 60
Dh 20 EVOLVESGGLVOPGSLRVSCAAGFASHYAMSVTRQAPGKLEWVAVISSGSGSTYY 79
Qy 61 SDSVKGRTISRDNKSLTLQMRSLAEDSAVYFCTR-VKL-----GTYYPDSW 109
Dh 80 ADSVKGRTISRDNKSLTLQMRSLAEDSAVYFCTR-VKL-----GTYYPDSW 139
Qy 110 GGGTLTVSSASTKGPVFLAPSSKSTSGTAAAGCLVDPPEPTVSMNSGALTSGV 169
Dh 140 GGGTLTVSSASTKGPVFLAPSSKSTSGTAAAGCLVDPPEPTVSMNSGALTSGV 199
Qy 170 HTTPAVLQSSGLYSLSSVTVPPSSSLGTQYICVNMHKPSNTKYDKKVPKSCDKHTYCP 229
Dh 200 HTTPAVLQSSGLYSLSSVTVPPSSSLGTQYICVNMHKPSNTKYDKKVPKSCDKHTYCP 259
Qy 230 PCPAPBLGGPSVFLFPPRKQDTLMSRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNA 289

Dh 260 PCPAPBLGGPSVFLFPPRKQDTLMSRTPEVTCVVVDVSHEDPEVKFNNYVDSGEVHNA 319
Qy 290 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 349
Dh 320 KTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 379
Qy 350 VYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYYKTPPTVLDSGSPFLY 409
Dh 380 VYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYYKTPPTVLDSGSPFLY 439
Qy 410 SKLTVDSKRWQGNVSPSCSYMEALNNHYTKSLSPGK 449
Dh 440 SKLTVDSKRWQGNVSPSCSYMEALNNHYTKSLSPGK 479

Search completed: December 23, 2004, 19:04:37
Job time : 163.904 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 28.813 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-54

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retrieval score: 366
Sequence: 1 DIQMTGSPSSLSASVGDRT.....HQYSKLPWTFGGTKWEIKR 108

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Scoring table: BLOSUM62

Searched: 2002273 reqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :
A: Genesepq.23sep04.*
1: Genesepq.1980s.*
2: Genesepq.1990s.*
3: Genesepq.2000s.*
4: Genesepq.2001s.*
5: Genesepq.2002s.*
6: Genesepq.2003as.*
7: Genesepq.2003bs.*
8: Genesepq.2004s.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	568	100.0	108	4	AAB81.988	Aab81.988 Gangliosid
	2	568	100.0	128	4	AAB81.999	Aab81.999 Gangliosid
	3	562	98.9	108	6	ABU11.011	Abu11.011 Modified
	4	561	98.8	128	4	AAB81.994	Aab81.994 Gangliosid
	5	555	97.7	128	4	AAB81.997	Aab81.997 Gangliosid
	6	551	97.0	128	4	AAB81.993	Aab81.993 Gangliosid
	7	548	96.5	108	4	AAB81.986	Aab81.986 Gangliosid
	8	545	96.0	128	4	AAB81.995	Aab81.995 Gangliosid
	9	545	96.0	128	4	AAB81.996	Aab81.996 Gangliosid
	10	544	95.8	128	4	AAB81.998	Aab81.998 Gangliosid
	11	532	93.7	128	4	AAB81.992	Aab81.992 Gangliosid
	12	514	90.5	108	4	AAB81.990	Aab81.990 Gangliosid
	13	514	90.5	108	6	ABU11.013	Abu11.013 Modified
	14	514	90.5	128	3	AAB81.928	Aab81.928 Mucin in
	15	514	90.5	128	4	AAB81.978	Aab81.978 Gangliosid
	16	514	90.5	128	6	ABU11.003	Abu11.003 Modified
	17	513	90.3	128	6	AAR31.257	Aar31.257 Ret Immun
	18	507	89.3	110	2	AAW70.673	Aaw70.673 Anti-VEGF
	19	507	89.3	110	5	ABP61.242	Abp61.242 Humaninsec
	20	507	89.3	237	2	AAW70.703	Aaw70.703 Protein e
	21	507	89.3	650	5	ABP61.241	Abp61.241 Phase-dia1
	22	506	89.1	128	2	AAV28.368	Aay28.368 pTM6d1 LTB
	23	505	88.9	107	2	AAW68.805	Aaw68.805 Variable
	24	505	88.9	107	2	AAW70.625	Aaw70.625 Humaninsec
	25	505	88.9	107	5	ABP61.194	Abp61.194 Humaninsec

ALIGNMENTS

26	504	88.7	110	2	AAW70675	Aaw70677 Ant1-VEGF
27	504	88.7	110	5	AAW61244	Abp61244 Humanised
28	503	88.6	108	2	AAW70618	Aaw70618 Ant1-VEGF
29	503	88.6	108	5	ADP61187	Adp61187 Humanised
30	503	88.6	108	8	ADG31782	Adg31782 V1L domain
31	503	88.6	108	8	ADG31768	Adg31768 V1L domain
32	503	88.6	108	8	ADG31893	Adg31893 V1L prot
33	503	88.6	110	3	AAW05897	Aaw05897 Humanised
34	503	88.6	110	3	AAH13376	Aah13376 F(ab)-12
35	501	88.2	107	2	AAW86804	Aaw86804 Variable
36	501	88.2	107	5	AAW70623	Aaw70623 Humanised
37	501	88.2	107	5	AAW61192	Abp61192 Humanised
38	500	88.0	108	8	ADG31770	Adg31770 V1L domain
39	500	88.0	110	2	AAW70677	Aaw70677 Ant1-VEGF
40	500	88.0	110	2	AAW70687	Aaw70687 Ant1-VEGF
41	500	88.0	110	5	AAH13380	Aah13380 Ant1-VEGF
42	500	88.0	110	5	ABP61256	Abp61256 Humanised
43	500	88.0	110	5	ADP61246	Adp61246 Humanised
44	500	88.0	214	7	ADG26154	Adg26154 Parent an
45	500	88.0	237	5	ABB81107	Abb81107 Ant1-VEGF

RESULT 1

ID	AAB81988 standard; protein, 108 AA.
XX	
AC	AAB81988;
XX	
D7	03-JUL-2001 (first entry)
XX	
DE	Ganglioside GD3 specific antibody related protein SEQ ID NO: 54.
XX	
KW	Ganglioside, GD3; complementarity determining region, CDR; antibody; cancer.
XX	
OS	Synthetic.
XX	
PN	WO200123432-A1.
XX	
PD	05-APR-2001.
XX	
FE	29-SEP-2000; 2000WO-JP006774.
XX	
FR	30-SEP-1999; 99JP-00278291.
PR	06-APR-2000; 2000JP-00105088.
XX	
PA	(KYOW) KYOMA HAKKO KOGYO KK.
XX	
PI	Hanai N, Shitara K, Nakamura K, Niwa R;
XX	
WI	WI; 2001-266143/27.
XX	
PT	New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.
PT	
PS	Claim 22; Page 172-173; 183pp; Japanese.
XX	
CC	The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
CC	
XQ	Sequence 108 AA;
Query Match	100.0%; Score 568; DB 4; Length 108;
Best Local Similarity	100.0%; Pred. No. 1.2e-35;
Matches 108; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 |||
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 |||
 QY 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
 |||
 DB 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
 |||

RESULT 2

AAB81999
 ID AAB81999 standard; protein; 128 AA.

AC AAB81999;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #8.

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 94JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

XX WPI; 2001-266143/27.

DR N-PSDB; AAF66913.

PT New human type complementation-determining region-transplanted antibody
 and derivatives against ganglioside GD3. The antibody and its derivatives are
 useful in the diagnosis and therapy of tumours, particularly cancer
 activity in cancer.

PS Example 1; Page 166; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react
 specifically with ganglioside GD3. The antibody and its derivatives are
 useful in the diagnosis and therapy of tumours, particularly cancer
 diagnosis. The present sequence is a protein used in the exemplification
 of the invention

XX Sequence 128 AA;

Query Match 100.0%; Score 568; DB 4; Length 128;

Best Local Similarity 100.0%; Pred. No. 1.4e-35;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 |||
 DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 80
 |||
 QY 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
 |||
 DB 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 128
 |||

RESULT 3

AAB11011

ID AAB11011 standard; protein; 108 AA.

XX

AC AAB11011;
 XX 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #4.

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Synthetic.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

XX WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3,
 its fragment, immunocompetent cell activators or/and antitumor agents in
 combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 100; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody
 against ganglioside GD3 or its fragment and at least 1 of a substance
 capable of activating immunocompetent cells and a substance having an
 antitumor activity in combination. The drugs can be used to treat tumour
 like melanoma and can provide a treatment with enhanced therapeutic
 effect and little side-reactions, particularly to relieve problems of
 side-effects during the conventional single administration. This sequence
 represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 108 AA;

Query Match 98.9%; Score 562; DB 6; Length 108;

Best Local Similarity 99.1%; Pred. No. 3.4e-35;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 |||
 DB 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQOKPDKAVKLLIFYSSNLHSGVPS 60
 |||
 QY 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
 |||
 DB 61 RFGSGSGTDYTLTISSLOPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
 |||

RESULT 4

AAB81994

ID AAB81994 standard; protein; 128 AA.

AC AAB81994;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein #3.

KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
 cancer.

OS Synthetic.

PN WO200123432-A1.

PD 05-APR-2001.

XX

```
PF 29-SEP-2000; 2000MO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
DR N-PSDB; AAF68898.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 155-156; 183pp; Japanese.
XX
XX PS The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX SQ Sequence 128 AA;

Query Match 98.8%; Score 561; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 4,7e-35;
Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCASQDISNNTLMWYQOKRPAKLLIFYSNLSHGVS 60
DB 21 DIQMTQSPSSLSASVGRVITTCASQDISNNTLMWYQOKRPAKLLIFYSNLSHGVS 80
QY 61 RFSGGSGSDYTLTITSSLPEDIAITYFCHQYSKLPMTFGGTKEIKR 108
DB 81 RFSGGSGSDYTLTITSSLPEDIAITYFCHQYSKLPMTFGGTKEIKR 128

RESULT 5
AAB81997
ID AAB81997 standard; protein; 128 AA.
XX
XX AAB81997;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein #6.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX OS Synthetic.
XX
XX PN WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX PD 29-SEP-2000; 2000MO-JP006774.
XX
XX PF 30-SEP-1999; 99JP-00278291.
XX
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PA Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
XX DR N-PSDB; AAF68907.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
```

```
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX PS Example 1; Page 161-162; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX SQ Sequence 128 AA;

Query Match 97.7%; Score 555; DB 4; Length 128;
Best Local Similarity 98.1%; Pred. No. 1.3e-34;
Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCASQDISNNTLMWYQOKRPAKLLIFYSNLSHGVS 60
DB 21 DIQMTQSPSSLSASVGRVITTCASQDISNNTLMWYQOKRPAKLLIFYSNLSHGVS 80
QY 61 RFSGGSGSDYTLTITSSLPEDIAITYFCHQYSKLPMTFGGTKEIKR 108
DB 81 RFSGGSGSDYTLTITSSLPEDIAITYFCHQYSKLPMTFGGTKEIKR 128

RESULT 6
AAB81993
ID AAB81993 standard; protein; 128 AA.
XX
XX AAB81993;
XX
XX 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein #2.
XX
XX KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX OS Synthetic.
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000MO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
XX
XX PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX PA Hanai N, Shitara K, Nakamura K, Niwa R;
XX WPI; 2001-266143/27.
XX
XX DR N-PSDB; AAF68895.
XX
XX PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX PS Example 1; Page 153; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX SQ Sequence 128 AA;

Query Match 97.0%; Score 551; DB 4; Length 128;
```

Best Local Similarity 97.2%; Pred. No. 2,7e-34;
Matches 105; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 80
QY 61 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
DB 81 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 128

RESULT 7

AAB81986
ID AAB81986 standard; protein; 108 AA.
XX

AC AAB81986;
XX

DT 03-JUL-2001 (first entry)
XX

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 10.
XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX

OS Synthetic.
XX

PN WO200123432-A1.
XX

PD 05-APR-2001.
XX

PF 29-SEP-2000; 2000WO-JP006774.
XX

PR 30-SEP-1999; 99JP-00278291.
XX

PR 06-APR-2000; 2000JP-00105088.
XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX

DR WPI; 2001-266143/27.
XX

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX

PS Example 1; Page 143-144; 183pp; Japanese.
XX

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX

SQ Sequence 108 AA;
XX

Query Match 96.5%; Score 548; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.9e-34;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 60
QY 61 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
DB 61 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108

RESULT 8

AAB81995
ID AAB81995 standard; protein; 128 AA.

XX AAB81995;
AC

DT 03-JUL-2001 (first entry)
XX

DE Ganglioside GD3 specific antibody related protein #4.
XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX

OS Synthetic.
XX

PN WO200123432-A1.
XX

PD 05-APR-2001.
XX

PF 29-SEP-2000; 2000WO-JP006774.
XX

PR 30-SEP-1999; 99JP-00278291.
XX

PR 06-APR-2000; 2000JP-00105088.
XX

PA (KYOW) KYOWA HAKKO KOGYO KK.
XX

PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX

DR WPI; 2001-266143/27.
XX

DR N-PSDB; AAF86901.
XX

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX

PS Example 1; Page 157-158; 183pp; Japanese.
XX

CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX

SQ Sequence 128 AA;
XX

Query Match 96.0%; Score 545; DB 4; Length 128;
Best Local Similarity 95.4%; Pred. No. 7.6e-34;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 60
DB 21 DIQMTQSPSSLSASVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSSNLHSGVPS 80
QY 61 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 108
DB 81 RPSGGSGTDYTLTITSLQPEDIAITYFCHQYSKLPMTFGQGTKEIKR 128

RESULT 9

AAB81996
ID AAB81996 standard; protein; 128 AA.

AC AAB81996;
XX

DT 03-JUL-2001 (first entry)
XX

DE Ganglioside GD3 specific antibody related protein #5.
XX

KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX

OS Synthetic.
XX

PN WO200123432-A1.
XX

PD 05-APR-2001.
XX
XX 29-SEP-2000; 2000MO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86904.
XX
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 159-160; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX
SQ Sequence 128 AA;

Query Match 96.0%; Score 545; DB 4; Length 128;
Best Local Similarity 95.4%; Pred. No. 7,6e-34;
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAVKLLIFYSNLSHGVP 80
QY 61 RFGGSGSGTDYTLTISLSLOPEDATYFCHQYSKLPFTFGGTKEIKR 108
DB 81 RFGGSGSGTDYTLTISLSLOPEDATYFCHQYSKLPFTFGGTKEIKR 128

RESULT 10
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
XX AAB81998;
AC
XX
XX 03-JUL-2001 (first entry)
DT
XX
XX Ganglioside GD3 specific antibody related protein #7.
DE
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
XX cancer.
XX
XX Synthetic.
OS
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000MO-JP006774.
PF
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX

PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 3; Page 164-165; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
XX
SQ Sequence 128 AA;

Query Match 95.8%; Score 544; DB 4; Length 128;
Best Local Similarity 96.3%; Pred. No. 9.1e-34;
Matches 104; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAVKLLIFYSNLSHGVP 60
DB 21 DIQMTQSPSSLSASVGDRTVITCSASQDISNYLNMWYQKPKAVKLLIFYSNLSHGVP 80
QY 61 RFGGSGSGTDYTLTISLSLOPEDATYFCHQYSKLPFTFGGTKEIKR 108
DB 81 RFGGSGSGTDYTLTISLSLOPEDATYFCHQYSKLPFTFGGTKEIKR 128

RESULT 11
AAB81992
ID AAB81992 standard; protein; 128 AA.
XX
XX AAB81992;
AC
XX
XX 03-JUL-2001 (first entry)
DT
XX
XX Ganglioside GD3 specific antibody related protein #1.
DE
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX
XX cancer.
XX
XX Synthetic.
OS
XX
XX WO200123432-A1.
PN
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000MO-JP006774.
PF
XX
XX 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX
XX WPI; 2001-266143/27.
DR N-PSDB; AAF86892.
XX
XX
XX New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX Example 1; Page 150-151; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumors, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX
SQ Sequence 128 AA;


```
FT Peptide 1. .20
FT /label= signal_peptide
PT Protein 21.128
FT /label= mature_immunoglobulin_light_chain_V_region
XX EP1013761-A2.
XX
XX
XX 28-JUN-2000.
XX
XX 18-SEP-1992; 99EP-00124345.
XX
XX 18-SEP-1991; 91JP-00238375.
XX
XX 18-SEP-1992; 92EP-00116026.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX WPI; 2000-402204/35.
XX
XX N-PSDB; AAA51004.
XX
XX
XX PT New humanized chimera antibody KM-871 useful for treating cancer,
XX PT comprises variable region of mouse monoclonal antibody, reactive with
XX PT ganglioside and human antibody constant region.
XX
XX Claim 14, Page 28-29; 65pp; English.
XX
XX
XX CC The present sequence is a murine immunoglobulin light chain variable
XX CC region from plasmid KM-641. The coding sequence was used in the creation
XX CC of an expression vector, along with the sequence for a human antibody, to
XX CC produce humanised chimaeric antibodies, which can be used to treat
XX CC cancer. Humanised chimaeric antibodies are more effective than mouse
XX CC antibodies as they do not provoke a reaction in the human and side
XX CC effects, such as the formation of anti-mouse immunoglobulin antibody and
XX CC the rapid half-life of the immunoglobulins, do not occur
XX
XX SQ Sequence 128 AA;
XX
XX
XX Query Match 90.5%; Score 514; DB 3; Length 128;
XX Best Local Similarity 88.9%; Pred. No. 1,7e-31;
XX Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 DIOMTQSPSSLSASVGDRTVTTCASQDISNYLWYQOKRDKAVKLLIFYSSNLHSGVPS 60
XX DB 21 DIOMTQASSLPASLDGRTVITSCASQDISNYLWYQOKRDKAVKLLIFYSSNLHSGVPS 80
XX
XX QY 61 RFSGGSGSDTYTTLTISLSLOPEDIATYFCHQYSKLPTWTFGGTKVEIKR 108
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 81 RFSGGSGSDTYTTLTISLSLEPEDIATYFCHQYSKLPTWTFGGTKVEIKR 128
XX
XX
XX RESULT 15
XX AAB81978
XX ID AAB81978 standard; protein; 128 AA.
XX
XX AC AAB81978;
XX
XX DT 03-JUL-2001 (first entry)
XX
XX DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 2.
XX
XX KM Ganglioside; GD3; complementarily determining region; CDR; antibody;
XX KM cancer.
XX
XX XX Mus musculus.
XX
XX OS Mus musculus.
XX
XX PN WO200123432-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 29-SEP-2000; 2000WO-JP006774.
XX
XX PR 30-SEP-1999; 99JP-00278291.
```

```
PR 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX
XX PT New human type complementation-determining region-transplanted antibody
XX PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX PT of e.g. tumors, with low antigenicity, little side effects but potent
XX PT activity in cancer.
XX
XX
XX PS Example 1; Page 140; 183pp; Japanese.
XX
XX CC The present invention describes a monoclonal antibody which can react
XX CC specifically with ganglioside GD3. The antibody and its derivatives are
XX CC useful in the diagnosis and therapy of tumors, particularly cancer
XX CC diagnosis. The present sequence is a protein used in the exemplification
XX CC of the invention
XX
XX SQ Sequence 128 AA;
XX
XX
XX Query Match 90.5%; Score 514; DB 4; Length 128;
XX Best Local Similarity 88.9%; Pred. No. 1,7e-31;
XX Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 DIOMTQSPSSLSASVGDRTVTTCASQDISNYLWYQOKRDKAVKLLIFYSSNLHSGVPS 60
XX DB 21 DIOMTQASSLPASLDGRTVITSCASQDISNYLWYQOKRDKAVKLLIFYSSNLHSGVPS 80
XX
XX QY 61 RFSGGSGSDTYTTLTISLSLOPEDIATYFCHQYSKLPTWTFGGTKVEIKR 108
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 81 RFSGGSGSDTYTTLTISLSLEPEDIATYFCHQYSKLPTWTFGGTKVEIKR 128
XX
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Search completed: December 23, 2004, 18:57:37
Job time : 29.8913 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 7.13276 Seconds
(without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568
Sequence: 1 D1QMTQSPSSLSASVDGRTV.....HOYSKLPMTFGGKTVKIKR 108

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patente AA:*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	90.5	128	4	US-09-225-322B-10
2	514	90.5	128	4	US-09-225-322B-19
3	514	90.5	128	4	US-09-764-304-10
4	514	90.5	128	4	US-09-764-304-19
5	503	88.6	110	4	US-09-440-781-94
6	491	86.4	108	3	US-09-065-059-3
7	487	85.7	127	3	US-08-649-100-33
8	484	85.2	124	1	US-08-458-516-12
9	481	84.7	110	4	US-09-440-781-95
10	480	84.5	107	2	US-07-934-373C-17
11	480	84.5	107	2	US-08-652-558-2
12	480	84.5	107	3	US-08-437-642B-17
13	480	84.5	107	3	US-08-146-206C-17
14	480	84.5	107	4	US-09-705-686-17
15	480	84.5	107	4	US-09-705-686-17
16	480	84.5	107	5	PCT-US93-07832-17
17	480	84.5	109	2	US-07-934-373C-47
18	480	84.5	109	3	US-08-437-642B-47
19	480	84.5	214	2	US-07-934-373C-40
20	480	84.5	214	2	US-08-788-800-11
21	480	84.5	214	3	US-08-437-642B-40
22	480	84.5	214	3	US-09-097-309-2
23	480	84.5	214	3	US-09-097-171A-2
24	480	84.5	214	3	US-09-460-587-2
25	480	84.5	214	3	US-09-940-166A-2
26	480	84.5	214	5	PCT-US93-07832-40
27	480	84.5	233	2	US-07-934-373C-25

28	480	84.5	233	3	US-08-437-642B-25	Sequence 25, Appl
29	480	84.5	233	4	US-08-146-206C-25	Sequence 25, Appl
30	480	84.5	233	4	US-09-705-686-25	Sequence 25, Appl
31	480	84.5	233	5	PCT-US93-07832-25	Sequence 25, Appl
32	480	84.5	237	3	US-09-097-309-6	Sequence 6, Appl
33	480	84.5	237	3	US-09-422-712B-2	Sequence 2, Appl
34	480	84.5	237	3	US-09-422-712B-2	Sequence 2, Appl
35	480	84.5	237	3	US-09-607-756-2	Sequence 2, Appl
36	480	84.5	237	3	US-09-460-587-6	Sequence 6, Appl
37	480	84.5	237	4	US-09-940-166A-6	Sequence 8, Appl
38	480	84.5	107	3	US-08-458-516-8	Sequence 1, Appl
39	479	83.8	107	3	US-09-254-189-1	Sequence 3, Appl
40	476	83.8	108	3	US-08-974-899-3	Sequence 3, Appl
41	475	83.6	108	4	US-09-795-798-3	Sequence 3, Appl
42	475	83.6	111	4	US-08-137-117D-67	Sequence 67, Appl
43	475	83.6	111	2	US-08-436-717-67	Sequence 67, Appl
44	475	83.6	126	1	US-08-137-117D-71	Sequence 71, Appl
45	475	83.6	126	1	US-08-137-117D-71	Sequence 71, Appl

ALIGNMENTS

```
RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIMURA, YOSHITAKA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; PRIOR APPLICATION NUMBER: 1999-01-05
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-09-225-322B-10

Query Match      90.5%; Score 514; DB 4; Length 128;
Best Local Similarity 88.9%; Pred. No. 1.2e-43;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Cy 1 D1QMTQSPSSLSASVDGRTVITCSAODISNLTNMQOKRPDKAVKLLIFYSSTLHGVPS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 D1QMTYTAASLPISLSDRGVITCSAODISNLTNMQOKRPDKAVKLLIFYSSTLHGVPS 80
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Cy RFSGGSGTDYTLTISSLOPEDIAATFCQYISKLPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 RFSGGSGTDYTLTISSLOPEDIAATFCQYISKLPWTFGGTKVEIKR 128
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
```


Sequence 94, Application US/09440781
Patent No. 6632926
GENERAL INFORMATION:
APPLICANT: Yvonne Man-ye Chen et al.
TITLE OF INVENTION: ANTIBODY VARIANTS
FILE REFERENCE: P146981
CURRENT APPLICATION NUMBER: US/09/440,781
CURRENT FILING DATE: 1999-11-16
NUMBER OF SEQ ID NOS: 99
SEQ ID NO 94
LENGTH: 110
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: artificial
LOCATION: 1-110
OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-94

Query Match 88.6%; Score 503; DB 4; Length 110;
Best Local Similarity 87.0%; Pred. No. 1.2e-42;
Matches 94; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 108

RESULT 6
US-09-065-059-3
Sequence 3, Application US/09065059
Patent No. 6068841

GENERAL INFORMATION:
APPLICANT: SEINO, Ken-ichiro
APPLICANT: KAYAGAKI, No. 6068841uhiko
APPLICANT: YAGITA, Hideo
APPLICANT: OKUMURA, Ko
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDermott, Will & Emery
STREET: 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,059
FILING DATE:
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Bucca Ph.D., Daniel
REGISTRATION NUMBER: P-42,368
REFERENCE/DOCKET NUMBER: 50356-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-518-5100
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-065-059-3

Query Match 86.4%; Score 491; DB 3; Length 108;
Best Local Similarity 84.3%; Pred. No. 1.9e-41;
Matches 91; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 108

RESULT 7
US-08-649-100-33
Sequence 33, Application US/08649100
Patent No. 6114507

GENERAL INFORMATION:
APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATSUE, TOMOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO. MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
METHOD OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-33

Query Match 85.7%; Score 487; DB 3; Length 127;
Best Local Similarity 86.0%; Pred. No. 5.6e-41;
Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 60
DB 21 DIQMTQSPSSLSASVGRVTITCSASODISNYLNMWYQOKPKAVKLIIFYSSNLHSGVPS 80
QY 61 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 107
DB 81 RFGSGSGTDYTLTISSLOPEDVATYFCHQYSKLPMTFGGTVEIKR 127

```
RESULT 8
US-08-458-516-12
; Sequence 12, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-08-458-516-12

Query Match      85.2%; Score 484; DB 1; Length 214;
Best Local Similarity 83.3%; Pred. No. 2e-40;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVRTITCSASODISNTLNTYQOKPKDAVKLLIFYSNLSHGVS 60
DB 1 DIQMTQSPSSLSASVDGVRTITCSASODISNTLNTYQOKPKDAVKLLIFYSNLSHGVS 60

QY 61 RFGSGSGTDYTLTISSLPEDIAIFYCHQYSKLPWTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDIPATYFCQCGNTLPTFTGGTVEIKR 108

RESULT 9
US-09-440-781-95
; Sequence 95, Application US/09440781
; Patent No. 6632926
; GENERAL INFORMATION:
; APPLICANT: Yvonne Man-yea Chen et al.
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: P1469R1
; CURRENT APPLICATION NUMBER: US/09/440,781
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 99
; SEQ ID NO 95
; LENGTH: 110
; TYPE: PRT
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; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: artificial
; LOCATION: 1-110
; OTHER INFORMATION: humanized antibody light chain variable domain
US-09-440-781-95

Query Match      84.7%; Score 481; DB 4; Length 110;
Best Local Similarity 81.5%; Pred. No. 1.9e-40;
Matches 88; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVRTITCSASODISNTLNTYQOKPKDAVKLLIFYSNLSHGVS 60
DB 1 DIQMTQSPSSLSASVDGVRTITCRANQGLSNTLNTYQOKPKDAVKLLIFYSNLSHGVS 60

QY 61 RFGSGSGTDYTLTISSLPEDIAIFYCHQYSKLPWTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISSLPEDIPATYFCQYSTVWTFGGTVEIKR 108

RESULT 10
US-07-934-373C-17
; Sequence 17, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/425-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino acid
; TOPOLOGY: linear
US-07-934-373C-17

Query Match      84.5%; Score 480; DB 2; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVRTITCSASODISNTLNTYQOKPKDAVKLLIFYSNLSHGVS 60
DB 1 DIQMTQSPSSLSASVDGVRTITCRASODIRNTLNTYQOKPKDAVKLLIYTSRLSGVS 60
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QY 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 107
DB 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 107

RESULT 11
US-08-652-558-2
Sequence 2, Application US/08652558
Patent No. 5861155
GENERAL INFORMATION:
APPLICANT: LIN, AUGUSTINE YEE-TIARN
TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER & WITCOFF
STREET: 75 STATE STREET, 23RD FLOOR
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,558
FILING DATE: JUNE 6, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB94/00387
FILING DATE: NOVEMBER 21, 1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, LEON R.
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,497-L
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-558-2

Query Match 84.5%; Score 480; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-40;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGRVTITCSASQDISNYLNMYQOKPKAVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCSASQDISNYLNMYQOKPKAVKLIIFYSSNLHSGVPS 60
QY 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 106
DB 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 106

RESULT 12
US-08-437-642B-17
Sequence 17, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-437-642B-17

Query Match 84.5%; Score 480; DB 3; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVDGRVTITCSASQDISNYLNMYQOKPKAVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCSASQDISNYLNMYQOKPKAVKLIIFYSSNLHSGVPS 60
QY 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 107
DB 61 RFGSGSGTDTYTLTSSLOPEDATYFCHQYSKLPMFTFGGTVEIK 107

RESULT 13
US-08-146-206C-17
Sequence 17, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)

;;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA: 07/715272
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-17

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Best Local Similarity 86.0%; Pred. No. 2.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Db 1 DIOMTSPSSLSASVGDRTVITCRASODIRNTLNTWYQKPKLIIYTSRLSGVPS 60

QY 61 RFSGGSGTDYTLTISLSLOPEDIATYFCHQYSKLPMTFGGTKEIK 107
Db 61 RFSGGSGTDYTLTISLSLOPEDPATYCCQGNLTLPMTFGGTKEIK 107

RESULT 14
US-09-705-686-17
; Sequence 17, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-NOV-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

;;
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-686-17

Query Match 84.5%; Score 480; DB 4; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Db 1 DIOMTSPSSLSASVGDRTVITCRASODIRNTLNTWYQKPKLIIYTSRLSGVPS 60

QY 61 RFSGGSGTDYTLTISLSLOPEDIATYFCHQYSKLPMTFGGTKEIK 107
Db 61 RFSGGSGTDYTLTISLSLOPEDPATYCCQGNLTLPMTFGGTKEIK 107

RESULT 15
US-09-705-392A-17
; Sequence 17, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-NOV-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-705-392A-17

Query Match 84.5%; Score 480; DB 4; Length 107;
Best Local Similarity 86.0%; Pred. No. 2.3e-40;
Matches 92; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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Db 1 DIOMTSPSSLSASVGDRTVITCRASODIRNTLNTWYQKPKLIIYTSRLSGVPS 60

QY 61 RFSGGSGTDYTLTISLSLOPEDIATYFCHQYSKLPMTFGGTKEIK 107

Db 61 RfSGSGSTDYTLTITSSLQPEDFATYYCQGNTLPMTRGQSTKVEIK 107

Search completed: December 23, 2004, 19:08:00
Job time : 17.1328 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 ; Search time 24.5684 Seconds
(Without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568

Sequence: 1 DQMTQSPKSLASVGRVT.....HOYSKLPWTGQGTKEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	514	90.5	128	9	US-09-764-304-19
3	514	90.5	128	14	US-10-265-713-10
4	514	90.5	128	14	US-10-265-713-19
5	514	90.5	128	14	US-10-166-626-10
6	514	90.5	128	14	US-10-166-626-19
7	507	89.3	110	9	US-09-056-1608-103
8	507	89.3	110	14	US-10-234-671-101
9	507	89.3	237	9	US-09-056-1608-100
10	507	89.3	237	14	US-10-234-671-100
11	507	89.3	491	13	US-10-011-125-2
12	505	88.9	107	9	US-09-056-1608-15
13	505	88.9	107	14	US-10-234-671-15

14	504	88.7	110	9	US-09-056-1608-105	Sequence 105, App
15	504	88.7	110	14	US-10-234-671-103	Sequence 103, App
16	503	88.6	108	9	US-09-056-1608-8	Sequence 8, App11
17	503	88.6	108	13	US-10-153-159-2	Sequence 2, App11
18	503	88.6	108	13	US-10-153-159-16	Sequence 16, App1
19	503	88.6	108	14	US-10-153-176-2	Sequence 2, App1
20	503	88.6	108	14	US-10-153-176-16	Sequence 16, App1
21	503	88.6	108	15	US-10-443-134A-2	Sequence 2, App1
22	503	88.6	108	15	US-10-443-134A-16	Sequence 16, App1
23	503	88.6	108	15	US-10-443-134A-127	Sequence 127, App
24	503	88.6	110	15	US-10-234-671-8	Sequence 8, App11
25	503	88.6	110	15	US-10-624-153-94	Sequence 94, App1
26	503	88.6	667	17	US-10-764-428-25	Sequence 25, App1
27	501	88.2	107	9	US-09-056-1608-13	Sequence 13, App1
28	501	88.2	107	14	US-10-234-671-13	Sequence 13, App1
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30	500	88.0	108	15	US-10-153-176-4	Sequence 4, App11
31	500	88.0	108	15	US-10-443-134A-4	Sequence 4, App11
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33	500	88.0	110	9	US-09-056-1608-117	Sequence 117, App
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35	500	88.0	110	14	US-10-234-671-115	Sequence 115, App
36	500	88.0	110	14	US-10-379-392-135	Sequence 135, App
37	500	88.0	213	16	US-10-379-392-137	Sequence 137, App
38	500	88.0	213	16	US-10-379-392-139	Sequence 139, App
39	500	88.0	214	14	US-10-364-953-1	Sequence 1, App11
40	500	88.0	237	14	US-10-020-786-10	Sequence 10, App1
41	500	88.0	667	17	US-10-764-428-7	Sequence 7, App1
42	500	88.0	667	17	US-10-764-428-13	Sequence 13, App1
43	500	88.0	670	17	US-10-764-428-5	Sequence 5, App11
44	500	88.0	670	17	US-10-764-428-9	Sequence 9, App11
45	500	88.0	670	17	US-10-764-428-11	Sequence 11, App1

ALIGNMENTS

RESULT 1

US-09-764-304-10

Sequence 10, Application US/09764304

Patent No. US20020026036A1

GENERAL INFORMATION:

APPLICANT: SHITARA, KENYA

APPLICANT: HANAI, NOBUO

APPLICANT: HASEGAWA, MAMORU

APPLICANT: MIYAJI, HIROMASA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

FILE REFERENCE: 249-101

CURRENT APPLICATION NUMBER: US/09/764,304

EARLIER FILING DATE: 2001-01-19

EARLIER APPLICATION NUMBER: 09/225,322

EARLIER FILING DATE: 1999-01-05

EARLIER APPLICATION NUMBER: US 08/454,680

EARLIER FILING DATE: 1995-05-31

EARLIER APPLICATION NUMBER: US 08/408,133

EARLIER FILING DATE: 1995-03-21

EARLIER APPLICATION NUMBER: US 08/292,178

EARLIER FILING DATE: 1994-08-17

EARLIER APPLICATION NUMBER: US07/947,674

EARLIER APPLICATION NUMBER: JP 3-238375

EARLIER FILING DATE: 1992-09-17

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10

LENGTH: 128

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: CDNA KM-641

US-09-764-304-10

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Query Match          90.5%; Score 514; DB 9; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.1e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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QY 61 RRSGGSGSDYTLTISLQPEDIAATYFCHQYSKLPMTFGGCTKVEIKR 108
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DB 81 RRSGGSGSDYTLTISLQPEDIAATYFCHQYSKLPMTFGGCTKVEIKR 128
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RESULT 2
US-09-764-304-19
; Sequence 19, Application US/09764304
; Patent No. US20020026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain
US-09-764-304-19

Query Match          90.5%; Score 514; DB 9; Length 128;
Best Local Similarity 88.9%; Pred. No. 7.1e-37;
Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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RESULT 3
US-10-265-713-10
; Sequence 10, Application US/10265713
; Publication No. US20030095964A1
; GENERAL INFORMATION:
; APPLICANT: SHITTARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; EARLIER APPLICATION NUMBER: US/09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; EARLIER APPLICATION NUMBER: US/09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: light chain
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OTHER INFORMATION: variable region
US-10-265-713-19

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Best Local Similarity	88.9%;	Pred. No. 7,1e-37;		
Matches	96;	Conservative	7;	Mismatches 5;
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RESULT5
US-10-166-626-10
; Sequence 10, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:

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APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAOMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUWANA, YOSHIOHSA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 229-101
CIPSOB NUMBER: 18740466 526

OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match	90.5%	Score 514;	DB 14;	Length 128;
Best Local Similarity	88.9%	Pred. No. 7.1e-37;		
Matches 96;	Conservative 7;	Mismatches 5;	Indels 0;	Gaps 0;

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; Sequence 19, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAOORU

APPLICANT: MIYAJI, HIROMASA
 APPLICANT: KIWANA, YOSHIHISA
 TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
 FILE REFERENCE: 249-101
 CURRENT APPLICATION NUMBER: US/10/166,626
 CURRENT FILING DATE: 2002-06-12
 PRIOR APPLICATION NUMBER: US/09/225,322B
 PRIOR FILING DATE: 1999-01-05
 PRIOR APPLICATION NUMBER: US 08/454,680
 PRIOR FILING DATE: 1995-05-31
 PRIOR APPLICATION NUMBER: US 08/408,133
 PRIOR FILING DATE: 1995-03-21
 PRIOR APPLICATION NUMBER: US 08/232,178
 PRIOR FILING DATE: 1994-08-17
 PRIOR APPLICATION NUMBER: US07/947,674
 PRIOR FILING DATE: 1992-09-17
 PRIOR APPLICATION NUMBER: JP 3-238375
 PRIOR FILING DATE: 1991-09-18
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 19
 LENGTH: 128
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:light chain
 US-10-166-626-19

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; OTHER INFORMATION: Description of Artificial Sequence:light chain
; OTHER INFORMATION: variable region
US-10-166-626-19

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Query Match	90.5%	Score 514	DB 14	Length 128
Best Local Similarity	88.9%	Pred. No. 7.1e-37		
Matches 96	Conservative 7	Mismatches 5	Indels 0	Gaps 0

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QY 61 RFSGGGSGIDYTLTISLQPEDIAFYCHQYSKLPWTFGGSTKEIKR 108
      |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 RFSGGGSGIDYSLTISLNEPEDIAFYCHQYSKLPWTFGGSTKEIKR 128

```

RESULT 7
US-09-056-160B-103
: Sequence 103 Application US/09056160B

Sequence 103, Application US/09056150B
Patent No. US2002003315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESSES:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-APR-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997

```
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-103

Query Match      89.3%; Score 507; DB 9; Length 110;
Best Local Similarity 88.0%; Pred. No. 2.5e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RRSGGSGSDTYTLTISLQPEDIAIFYCHQYSKLPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RRSGGSGSDTYTLTISLQPEDFATYYCQQYSTVPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-10-234-671-101
Sequence 101, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: Amino Acid
```

```
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-234-671-101

Query Match      89.3%; Score 507; DB 14; Length 110;
Best Local Similarity 88.0%; Pred. No. 2.5e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RRSGGSGSDTYTLTISLQPEDIAIFYCHQYSKLPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 RRSGGSGSDTYTLTISLQPEDFATYYCQQYSTVPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-09-056-160B-100
Sequence 100, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-100

Query Match      89.3%; Score 507; DB 9; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.3e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 DIQMTQSPSSLSASVDGDRVTITCSASQDISNTLNMVYQQRKPAVKLLIFYSNLSHGVS 83
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 RRSGGSGSDTYTLTISLQPEDIAIFYCHQYSKLPWTFGGTKVEIKR 108
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 RRSGGSGSDTYTLTISLQPEDFATYYCQQYSTVPWTFGGTKVEIKR 131
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 10
US-10-234-671-100
Sequence 100, Application US/102334671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cu1, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-234-671-100
Query Match 89.3%; Score 507; DB 14; Length 237;
Best Local Similarity 88.0%; Pred. No. 5.3e-36;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCSAGODISNYLNMTQOKPKDKAVKLLIFYSNLSHGVP 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAGODISNYLNMTQOKPKDKAVKLLIFYSNLSHGVP 83
QY 61 RFSGGSGGTDYTLTISLQPEDIAFYFCHQYSKLPMTFGGTVEIKR 108
DB 84 RFSGGSGGTDYTLTISLQPEDIAFYFCHQYSKLPMTFGGTVEIKR 131
RESULT 11
US-10-011-125-2
Sequence 2, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1

CURRENT APPLICATION NUMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
US-10-011-125-2
Query Match 89.3%; Score 507; DB 13; Length 491;
Best Local Similarity 88.0%; Pred. No. 1.1e-35;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCSAGODISNYLNMTQOKPKDKAVKLLIFYSNLSHGVP 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAGODISNYLNMTQOKPKDKAVKLLIFYSNLSHGVP 83
QY 61 RFSGGSGGTDYTLTISLQPEDIAFYFCHQYSKLPMTFGGTVEIKR 108
DB 84 RFSGGSGGTDYTLTISLQPEDIAFYFCHQYSKLPMTFGGTVEIKR 131
RESULT 12
US-09-056-160B-15
Sequence 15, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-15
Query Match 88.9%; Score 505; DB 9; Length 107;
Best Local Similarity 88.8%; Pred. No. 3.6e-36;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 : Search time 5.83589 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568
Sequence: 1 DIQWTQSPSSLSASVGRVT.....HQYSKLPWTGQTKVEIKR 108

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	84.5	108	1 KIHUAV	Ig kappa chain V-I
2	479	84.3	111	2 A38740	Ig kappa chain V r
3	477	84.0	111	2 E38740	Ig kappa chain V r
4	472	83.1	111	2 G38740	Ig kappa chain V r
5	469	82.6	111	2 C38740	Ig kappa chain V r
6	466	82.0	107	2 B49026	Ig kappa chain V r
7	462	81.3	127	2 S40367	Ig kappa chain V-J
8	461	81.2	108	1 KWS73	Ig kappa chain V r
9	461	81.2	108	1 KWS73	Ig kappa chain V r
10	456	80.3	108	1 KIHURE	Ig kappa chain V-I
11	454	79.9	122	2 A29380	Ig kappa chain pre
12	452	79.6	108	2 S69903	Ig kappa chain (cl
13	452	79.6	115	2 UJ0080	Ig kappa chain pre
14	451	79.4	129	2 S52789	Ig kappa chain V r
15	450	79.2	110	2 S44118	Ig kappa chain V-J
16	448	78.9	108	1 KYMSAR	Ig kappa chain V r
17	447	78.7	108	1 S69902	Ig kappa chain (cl
18	447	78.7	109	2 PH0888	Ig kappa chain V r
19	447	78.7	126	2 A34904	Ig kappa chain pre
20	445	78.3	108	1 KIHUAG	Ig kappa chain V-I
21	445	78.3	108	2 I39154	Ig kappa chain (BR
22	445	78.3	125	2 S40333	Ig kappa chain V-J
23	444	78.2	108	2 A26406	Ig kappa chain V r
24	443.5	78.1	107	2 S69901	Ig kappa chain (cl
25	443	78.0	139	2 S40365	Ig kappa chain - h
26	442	77.8	123	2 S40352	Ig kappa chain - h
27	442	77.8	131	2 S40352	Ig kappa chain V-J
28	441.5	77.7	108	2 S38862	Ig kappa chain V r
29	441	77.6	108	2 B49047	Ig kappa chain V r

30	440	77.5	107	2 A48677	Ig kappa chain V-J
31	439	77.3	108	2 S44122	Ig kappa chain V r
32	439	77.3	108	2 C26405	Ig kappa chain V r
33	438	77.1	108	1 KIHURV	Ig kappa chain V-I
34	438	77.1	108	2 S19970	Ig kappa chain V r
35	437.5	77.0	107	2 S36275	Ig kappa chain V r
36	437	76.9	107	2 B48677	Ig kappa chain V-J
37	437	76.9	107	2 B28044	Ig kappa chain V r
38	436	76.8	108	2 P10282	Ig kappa chain V r
39	435	76.6	109	2 S31998	Ig kappa chain - h
40	434	76.4	107	2 S36264	Ig kappa chain V
41	434	76.4	107	2 A28044	Ig kappa chain V r
42	433	76.2	107	2 D48677	Ig kappa chain V-J
43	433	76.2	108	1 KIHURE	Ig kappa chain V-I
44	433	76.2	108	2 B26405	Ig kappa chain V r
45	433	76.2	127	2 PH1224	Ig kappa chain pre

ALIGNMENTS

RESULT 1

KIHUAV

Ig kappa chain V-I region (Au) - human

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence: revision 02-Jul-1998 #text_change 09-Jul-2004

C:Accession: A91653; A01862; S02573

R:Schleich, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972

A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Su

A:Reference number: A91653; MUID:72189444; PMID:5028201

A:Accession: A91653

A:Molecule type: protein

A:Residues: 1-108 <SCH>

A:Cross-references: UNIPROT:P01594

A:Note: The C region of this chain has the Inv (3) marker

R:Feilhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Ste

Biophys. Struct. Mech. 1, 139-146, 1975

A:Title: The structure determination of the variable portion of the Bence-Jones protein

A:Reference number: A90729; MUID:77022433; PMID:1234024

A:Contents: annotation; X-ray crystallography

A:Note: the structure of the V region was determined by molecular replacement methods u

R:Steiner, V.; Chang, J.Y.

FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances th

A:Reference number: S02572; MUID:88005152; PMID:3115831

A:Contents: annotation

C:Comment: This is a Bence Jones protein.

C:Genetics:

A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotrimer subunit consists of two identical light (ka

hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IPM>

F:23-88/Disulfide bonds: #status predicted

Query Match 84.5% Score 480; DB 1; Length 108;

Best local similarity 85.2% Pred. No. 1.7e-36;

Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQWTQSPSSLSASVGRVTITTSASQDISNYLWYQOKPKAVKLLIFYSNLSGVP 60

Db 1 DIQWTQSPSSLSASVGRVTITTSASQDISNYLWYQOKPKAVKLLIFYSNLSGVP 60

QY 61 RFSGGSGCTDYTLTSSLOPEDATYFCHQYSKLPWTFGGTVEIKR 108

Db 61 RFSGGSGAHFTTSSLOPEDATYVCOQDYLVPTFGGTVEIKR 108

QY 61 RFSGGSGAHFTTSSLOPEDATYVCOQDYLVPTFGGTVEIKR 108

Db 61 RFSGGSGAHFTTSSLOPEDATYVCOQDYLVPTFGGTVEIKR 108

RESULT 2

A:Reference number: PLo0220; NCID:90278348; PMID:1693654
A:Accession: PLo0220
A:Stratus: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <PUC>
A:Experimental source: strain lupus-Prone MRL-lpr/lpr mouse
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:50-56/Region: complementarity-determining 2
F:89-97/Region: complementarity-determining 3

Query Match	82.0%;	Score 466;	DB 2;	Length 107;
Best Local Similarity	82.2%;	Pred. No. 3.1e-35;		
Matches	88;	Conservative	10;	Mismatches 9;
			Indels	0;
			Gaps	0;

OY

1 DIQMTPSSSLASVGRVTITCSAQDPSINLYNQKDKAVKLIFYSNLTGVS 60
||||| : ||||| : ||||| : ||||| : |||||
Dd

1 DIRMOTTSLSASLGPRVTISCRASQDISNYLWYQQKPDTVKLLIYYTSLHGSVP 60

```

QY      61 RFSGGSGSTDYTLTIISSLPEDIATYFCHQSKLPMTFGGQSTKVEIK 107
        |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RFSGGSGSTDYSLTISLNLEPEDIATYCCQSKLPRTFGGQSTKEIK 107

```

RESULT 7
S40367
Ig kappa chain V-J-C region - human

CiDate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiAccession: S40367
C:Klein, R.; Jaenichen, R.; Zachau, H.G.
Date: 1994-05-19
Date: 1995-05-26
Date: 2000-01-21

A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown

A:Residues: 1-127 <KLIE>
A:Cross-references: EMBL:X72477
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
E/33-107/Domain: Immunoglobulin homology <IMM>

Query Match	81.3%	Score 462;	DB 2;	Length 127;
Best Local Similarity	82.4%;	Pred. No. 8.6e-35;		
Matches 89; Conservative	6;	Mismatches 13;	Indels 0;	Gaps 0;

QY 1 DIQMTPSSLSASVGDRTVITCSASQDISNLYLMWYQKPKDKAVKLLIFSSNLSHGVPSS 60
 18 DIQMTPSSLSASVGDRTVITCRASQDISNLYLMWYQKPKDKAVKLLIYAASSLSGVPSS 77

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Qy      61 RFSGGSGSTDTLTITSSLDGEDIATYFCHQYSKLPWTFGGTKVEIKR 108
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      78 RFSGSGSGSTDTLTITSSLDGEDFATYVCCQSYNTPWTFGGTKVEIKR 125

```

RESULT 8
KVMS73

```
C:\Species: Mus musculus (house mouse)
C:\Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:\Accession: A01926
```

Eur. J. Biochem. 59, 525-537, 1975
 A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid
 A:Reference number: A01926; PMID:76091934; PMID:812696

A/Residues: 1-108 <SCH>
A/Cross-references: UNIPROT:P01643
C/Comment: This chain was isolated from a myeloma protein

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 chain disulfide bonds.
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
E:16-90/Domain: Immunoglobulin homology <Imm>
F:23-88/Disulfide bonds: #status predicted

Query Match	81.2%;	Score 461;	DB 1;	Length 108;
Best Local Similarity	78.7%;	Pred. No. 9e-35;		
Matches	85;	Conservative	13;	Mismatches 10;
				Gaps 0;

Qy 1 DIQMTQSPSSLSASVDGRTVITCSASQDISNTLNWYQKPKDKAVKLLIFSSNNLHSGVPS 600

Db 1 DIQMTQTSSLSASLGDRTVITCSASQSIGNYLBWYQKPKDGTVKLLIYYTSSLHSGVPS 600

QY 61 RFGSGSGSDYTLTISLQPDIAITYFCHQYSKLPWTFGGTKVEIKR 108
 |||||:|||||:::|||||:|||||:|||||
 Db 61 RFGSGSGSDYSLTISBLPZBIATYYCOYSKLPRTFGGTKLEIKR 108

RESULT 9
S69900
Ig kappa chain (clone KJ.2.18 / KL4B10 / KL4C11) - mouse

C.Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C.Accession: S69900; S69907; S69908
C.Wysocki, L.J.; Creighton, G.; Lehmann, K.R.; Cambier, J.C.
Tamura, K. 75 116-121 1993

A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69900
A:Status: preliminary; translation not shown

A1:Cross-references: EMBL:X55041; NID:g511023; PIDN:CAA38881.1; PID:g511024
A1:Accession: S69907
A1:Status: preliminary; translation not shown

AiCross-references: EMBL:X55048; NID:g511037; PIDN:CAA38888.1; PID:g511038
 AiAccession: S69908
 AiStatus: preliminary; translation not shown

A:Cross-references: EMBL:X55049; NID:g511039; PIDN:CAA38889.1; PID:g511040
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <1MM>

Query Match	81.2%	Score 461	DB 2	Length 108
Best Local Similarity	80.6%	Pred. No. 9e-35		
Matches 87	Conservative 10	Mismatches 11	Indels 0	Gaps 0

```

Oy      1 DIGNTQSPSSLSASVGDRTVITTCASAGODISNLTNMYQOKPDKAVKLLIFYSSNTHSGVPS 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 DIGNTQTTSLSASLGDRVTISCRASODISNLTNMYQOKPDGTVYKLLIYTSRLHSGVPS 60

```

```

Oy      61 RFGSGSGSDYTLTITSSLPEDIAATYFCHQYSKLPWTFGGGTKEIKR 108
      ||| ||| ||| : ||| : ||| ||| : ||| ||| : |||
Db      61 RFGSGSGSDYSLTISNLEQEDIAATYFCQGGNTLPWTFGGGTKEIKR 108

```

RESULT 10
KIHURE
IG kappa

CjDate: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
CjAccession: A91663; A01873
RjPalm, W.; Hilschmann, N.

vollständige Aminosäuresequenz des Proteins.
A:Reference number: A91663; MUID:76023758; PMID:809329
A:Accession: A91663

A:Molecule type: protein
A:Residues: 1-108 <PAL>
A:Cross-references: UNIPROT:P01607
A>Note: the C region of this chain has the Inv (1,2) marker
R:BDP, O.; Lactman, E.B.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A:Title: The molecular structure of a dimer composed of the variable portions of the Bar
A:Reference number: A90392; MUID:76039968; PMID:1182131
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2P12-2P12
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (key
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status experimental

Query Match 80.3%; Score 456; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 2,5e-34;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
Db 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60

QY 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
Db 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108

RESULT 11

IG kappa chain precursor V region (AC-1001) - mouse (fragment)
A29380
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: A29380
R:Chen, H.T.; Kabat, E.A.; Lumbiad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A:Reference number: A92612; MUID:88007582; PMID:3115981
A:Accession: A29380
A:Molecule type: mRNA
A:Residues: 1-122 <CHE>
A:Cross-references: GB:M17160; GB:J02815; NID:g196895; PTDN:AAA38824.1; PID:g196896
A>Note: the authors translated the codon TTC for residue 1 as Leu
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 79.9%; Score 454; DB 2; Length 122;
Best Local Similarity 79.6%; Pred. No. 4,3e-34;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
Db 15 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 74

QY 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
Db 75 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 122

RESULT 12

S69903
IG kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Wysocki, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.

Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69903
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55044; NID:g511029; PTDN:CAA38884.1; PID:g511030
A:Accession: S69904
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55045; NID:g511031; PTDN:CAA38885.1; PID:g511032
A:Accession: S69905
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55046; NID:g511033; PTDN:CAA38886.1; PID:g511034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 452; DB 2; Length 108;
Best Local Similarity 79.6%; Pred. No. 5,8e-34;
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
Db 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60

QY 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
Db 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108

RESULT 13

IG kappa chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)
JL0080
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0080
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A:Reference number: JL0076; MUID:8906973; PMID:3211160
A:Accession: JL0080
A:Molecule type: mRNA
A:Residues: 1-115 <KAA>
A:Cross-references: GB:M27793; NID:g197161; PTDN:AAA38937.1; PID:g197162
A>Note: the authors translated the codon ACG for residue 30 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F:7-115/Product: Ig light chain #status predicted <MRT>
F:22-96/Domain: immunoglobulin homology <IMM>
F:30-40/Region: complementarity-determining 1
F:56-62/Region: complementarity-determining 2

Query Match 79.6%; Score 452; DB 2; Length 115;
Best Local Similarity 79.6%; Pred. No. 6,2e-34;
Matches 86; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
1 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 60
Db 7 DIOMTQSPSLASVGVDRVTITCSASQDISNYLNMWYQKRPDKAVKLLIFYSNLSHGVS 66

QY 61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
61 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 108
Db 67 RFGSGSGTDYTLTISLSLOPEDIAITYFCHQYSKLPMTFGGQTKVEIKR 114

RESULT 14

S52789
IG kappa chain V region - human (fragment)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 30.044 Seconds

(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-54

Perfect score: 568
Sequence: 1 DQMTQSPSSLSASVGRVT.....HQYSKLPWTRGQGKVKIKR 108

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	480	84.5	108	1 KVI1B_HUMAN	P01594 homo sapien
2	465	81.9	233	2 Q91WS9	Q91WS9 mus musculu
3	461	81.2	108	1 KVSJ_MOUSE	P01643 mus musculu
4	461	81.2	234	2 Q8R062	Q8R062 mus musculu
5	456	80.3	108	1 KVI1O_HUMAN	P01607 homo sapien
6	454	79.9	111	2 AAR10992	Aar10992 mus muscu
7	448	78.9	108	1 KVSJ_MOUSE	P01644 mus musculu
8	447	78.7	108	1 KVSJ_MOUSE	P01645 mus musculu
9	447	78.7	108	1 KVSJ_MOUSE	P01646 mus musculu
10	445	78.3	108	1 KVI1A_HUMAN	P01593 homo sapien
11	445	78.3	108	1 KVSJ_MOUSE	P01648 mus musculu
12	445	78.3	108	2 Q9UL77	Q9UL77 homo sapien
13	443	78.0	108	1 KVSJ_MOUSE	P01647 mus musculu
14	439	77.3	236	2 Q6GMF1	Q6GMF1 homo sapien
15	438	77.1	108	1 KVI1P_HUMAN	P01608 homo sapien
16	436	76.8	108	1 KVI1Y_HUMAN	P016362 homo sapien
17	434	76.4	108	1 Q9UL70	Q9UL70 homo sapien
18	433.5	76.3	107	2 Q96SA9	Q96SA9 homo sapien
19	433	76.2	108	1 KVI1R_HUMAN	P01649 homo sapien
20	433	76.2	234	2 Q91WF8	Q91WF8 mus musculu
21	433	76.2	236	2 Q6GMX9	Q6GMX9 homo sapien
22	430	75.7	108	1 KVSJ_MOUSE	P01646 mus musculu
23	430	75.7	107	2 Q7Z3Y4	Q7Z3Y4 homo sapien
24	429	75.5	107	2 Q9UL84	Q9UL84 mus musculu
25	429	75.5	108	1 KVI1M_HUMAN	P01605 homo sapien
26	427	75.2	236	2 Q6GMX8	Q6GMX8 homo sapien
27	425	74.8	103	2 AAR11052	Aar11052 mus muscu
28	424	74.6	108	1 KVI1H_HUMAN	P01600 homo sapien
29	423	74.5	236	2 Q6GMX0	Q6GMX0 homo sapien
30	422	74.3	129	1 KVI1W_HUMAN	P04433 homo sapien
31	420	73.9	108	1 KVI1K_HUMAN	P01603 homo sapien

32	420	73.9	108	1 KVI1Q_HUMAN	P01609 homo sapien
33	419	73.8	108	1 KVI1V_HUMAN	P04430 homo sapien
34	418	73.6	108	1 KVI1L_HUMAN	P01604 homo sapien
35	417	73.4	108	1 KVI1C_HUMAN	P01593 homo sapien
36	416.5	73.3	107	2 Q9UL81	Q9UL81 homo sapien
37	416	73.2	108	1 KVI1N_HUMAN	P01606 homo sapien
38	416	73.2	116	2 Q96PF6	Q96PF6 homo sapien
39	414	72.9	236	2 Q6PIH7	Q6PIH7 homo sapien
40	414	72.9	236	2 AAR34141	Aar34141 homo sapi
41	413	72.7	108	1 KVI1S_HUMAN	P01611 homo sapien
42	412	72.5	108	1 KVI1G_HUMAN	P01599 homo sapien
43	411	72.4	108	1 KVI1E_HUMAN	P01597 homo sapien
44	411	72.4	234	2 Q7Z473	Q7Z473 homo sapien
45	408.5	71.9	107	1 KVI1D_HUMAN	P01596 homo sapien

ALIGNMENTS

RESULT 1
KVI1B_HUMAN STANDARD; PRT; 108 AA.
ID KVI1B_HUMAN
AC P01594;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 1g kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE.
RP MEDLINE=72189444; Pubmed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
RT Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; Pubmed=1234024;
RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RT Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: The structure of the V region was determined by molecular replacement methods using the known structure of the V region of the kappa chain RSI.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC PIR; A91653; KIHUAV.
DR PDB; 1JVS; X-ray; A=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5

FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 44 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6B9 CRC64;

Query Match 84.5%; Score 480; DB 1; Length 108;
 Best Local Similarity 85.2%; Pred. No. 9.5e-43;
 Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTVITCSAQDISNTLNTMYQKPKDKAVKLLIFYSNLSHGVP 60
 Db 1 DIQMTSPSSLSASVGDRTVITCSAQDISNTLNTMYQKPKDKAVKLLIFYSNLSHGVP 60
 Qy 61 RFGSGSGSDYTLTITSLQPEDIAITYFCHQYSKLPMTFGGKVEIKR 108
 Db 61 RFGSGSGAHFTTITSLQPEDIAITYCOQYDYLPMFTFGGKVEIKR 108

RESULT 2.

ID Q91WS9 PRELIMINARY; PRT; 233 AA.
 AC Q91WS9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DIC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; Pubmed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravinsky M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;

RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013496; AAH13496.1; -.
 DR PIR; A38740; A38740.
 DR PIR; C38740; C38740.
 DR PIR; E38740; E38740.
 DR PIR; G38740; G38740.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00654; Cl-set; 1.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 81.9%; Score 465; DB 2; Length 233;
 Best Local Similarity 79.6%; Pred. No. 9.2e-41;
 Matches 86; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTVITCSAQDISNTLNTMYQKPKDKAVKLLIFYSNLSHGVP 60
 Db 20 DIQMTTSSLSASVGDRTVITCSAQDISNTLNTMYQKPKDKAVKLLIFYSNLSHGVP 79
 Qy 61 RFGSGSGSDYTLTITSLQPEDIAITYFCHQYSKLPMTFGGKVEIKR 108
 Db 80 RFGSGSGSDYTLTITSLQPEDIAITYCOQYRXLPMFTFGGKVEIKR 127

RESULT 3

ID KVSJ_MOUSE STANDARD; PRT; 108 AA.
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region MOPC 173.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
 RC MEDLINE=76091934; Pubmed=812696;
 RA Schilt C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin. Amino-acid sequence of the light chain.";
 RL Eur. J Biochem. 59:525-537(1975).
 RC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
 DR PIR; A01926; KWS73.
 DR HSSP; P01594; IJVS.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Framework-2.
 FT DOMAIN 35 49 Framework-3.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 108 Framework-4.
 FT DISUFID 23 88 By similarity.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72A0A3 CRC64;

Query Match 81.2%; Score 461; DB 1; Length 108;


```

FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
RX STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 80.3%; Score 456; DB 1; Length 108;
Best Local Similarity 80.6%; Pred. No. 3.2e-40;
Matches 87; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 60

QY 61 RFGSGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 108

RESULT 6
AAR10992 PRELIMINARY; PRT; 111 AA.
AC AAR10992;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DE AHA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY346832; AAR10992.1; -.
FT NON TER 1 1
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12120 MW; 879A9DB5880C59D CRC64;

Query Match 79.9%; Score 454; DB 2; Length 111;
Best Local Similarity 81.0%; Pred. No. 5.5e-40;
Matches 85; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 4 MTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 63
DB 1 MTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 60

QY 64 GGGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 108
DB 61 GGGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 105

RESULT 7
KV5K MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR PIR; A01927; KYMSAR.
DR HSSP; P01594; 1UV5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 78.9%; Score 448; DB 1; Length 108;
Best Local Similarity 79.6%; Pred. No. 2.3e-39;
Matches 86; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 60
DB 1 DIOMTQSPSSLSASVGDRTVITCSASQDISNLTNMTYQKPKLVKLLIFSSNLTSGVPS 60

QY 61 RFGSGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 108
DB 61 RFGSGSGTDYTLTISLSQPEDIAITYFCHQYSKLPFTFGGTVEIKR 108

RESULT 8
KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG kappa chain V-V region HP 9367.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idioType."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

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FT	DOMAIN	57	56	Complementarity-determining-2.
FT <td>DOMAIN</td> <td>57</td> <td>56</td> <td>Complementarity-determining-2.</td>	DOMAIN	57	56	Complementarity-determining-2.
FT <td>DOMAIN</td> <td>89</td> <td>97</td> <td>Complementarity-determining-3.</td>	DOMAIN	89	97	Complementarity-determining-3.
FT <td>DOMAIN</td> <td>98</td> <td>108</td> <td>Complementarity-determining-4.</td>	DOMAIN	98	108	Complementarity-determining-4.
FT <td>DISULFID</td> <td>23</td> <td>88</td> <td>By similarity.</td>	DISULFID	23	88	By similarity.
FT <td>NON_TER</td> <td>108</td> <td>108</td> <td></td>	NON_TER	108	108	
SO <td>SEQUENCE</td> <td>108 AA;</td> <td>11954 MW;</td> <td>22F4642C63EFP58E CRC64;</td>	SEQUENCE	108 AA;	11954 MW;	22F4642C63EFP58E CRC64;
Query Match				
Best Local Similarity		78.7%;	Score 447;	DB 1; Length 108;
Matches		86; Conservative	10; Mismatches	12; Indels 0; Gaps 0;
Qy	1	DIQMTPSSLSASAGDRTYTICSA	SODISNTLNMYYQOKPDKAVKLLIFYSNLSHGVPS	60
Db	1	DIQMTPSSLSASAGDRTYTICSA	SODISNTLNMYYQOKPDKAVKLLIFYSNLSHGVPS	60
Qy	61	RFGSGSGSTDYTLTISNLEQED	IATYFCQQGYMLPRTEGGKRLIKR	108
Db	61	RFGSGSGSTDYTLTISNLEQED	IATYFCQQGYMLPRTEGGKRLIKR	108
Qy	61	RFGSGSGSTDYTLTISNLEQED	IATYFCQQGYMLPRTEGGKRLIKR	108
Db	61	RFGSGSGSTDYTLTISNLEQED	IATYFCQQGYMLPRTEGGKRLIKR	108

RESULT 10	KYLA HUMAN	STANDARD	PRT	108 AA
AC	P01593;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig kappa chain V-I region AG.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=69324734; PubMed=4893682;			
RA	Tilani K., Shinoda T., Putnam P.W.;			
RT	"The amino acid sequence of a kappa type Bence-Jones protein. 3. The			
RT	complete sequence and the location of the disulfide bridges."			
RL	J. Biol. Chem. 244:3550-3560(1969).			
CC	-1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.			
CC	-1- MISCELLANEOUS: This is a Bence-Jones protein.			
DR	PIR, A01861; K1HDAG.			
DR	HSSP; P01607; IBMW.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006985; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG LIKE; 1.			
KM	Bence-Jones protein; Direct protein sequencing;			
KV	Immunoglobulin V region.			
FT	DOMAIN 1 23 Framework-1.			
FT	DOMAIN 24 34 Complementarity-determining-1.			
FT	DOMAIN 35 49 Framework-2.			
FT	DOMAIN 50 56 Complementarity-determining-2.			
FT	DOMAIN 57 88 Framework-3.			
FT	DOMAIN 89 97 Complementarity-determining-3.			
FT	DOMAIN 98 107 Framework-4.			
FT	DISULFID 23 88			
FT	NON TER 108 108			
SQ	SEQUENCE 108 AA; 11592 MW; E33B3246C18F0C4F CRC64;			
Query Match	78.3%; Score 445; DB 1; Length 108;			
Best Local Similarity	78.7%; Pred. No. 4.7e-39;			
Matches	85; Conservative 9; Mismatches 14; Indels 0; Gaps 0;			
QY	1 DIQNTQSSSSISAVGDRVTTCGASQSDISNYLWYQOKPKDAVKLLIFYSNNHSGVPS 60			
DB	1 DIQNTQSSSSISAVGDRVTTCGASQSDINNYLWYQGGPKAKKILIDYDSNNLETGVP 60			
QY	61 RPSGGSGSTDTYTLTSSIQPEPDITTYFCHQYSKLPWTFGGCTKVEIKR 108			
DB	61 RPSGGSGFETDPTFTISGLQPEDITATYVCOQYDTLPRTFGGCTKLEIKR 108			
RESULT 11				
KV50_MOUSE	STANDARD;	PRT;	108 AA.	
AC	P01648;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig kappa chain V-V region HP 51AA.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=A/J;			

RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idio type.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP: P01594; 1JVS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDASE9A45291C CRC64;

Query Match 78.3%; Score 445; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 4,7e-39;
Matches 84; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
Db 61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108

RESULT 12
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
ID Q9UL77;
AD 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=6614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RU Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -.
DR PIR: B49047; B49047.
DR PIR: S34083; S34083.
DR HSSP: P01607; 1BMW.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C066B1716CAD16F3 CRC64;

Query Match 78.3%; Score 445; DB 2; Length 108;

Best Local Similarity 79.6%; Pred. No. 4,7e-39;
Matches 86; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
Db 61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108

RESULT 13
KVSN_MOUSE STANDARD; PRT; 108 AA.
ID KVSN_MOUSE
AC P01677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idio type.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSSP: P01607; 1REI.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFBA2 CRC64;

Query Match 78.0%; Score 443; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 7,7e-39;
Matches 85; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
Db 1 DIQMTPSSLSASVGDRTTTCASQDISNLTNMYQQKPKAVKLLIFYSNLSHGVS 60
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
Db 61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108
61 RFGSGSGSDYTLTISLQPEDIATYFCHQYKLPWTFQGTRKVEIKR 108

RESULT 14
O6GMW1 PRELIMINARY; PRT; 236 AA.
ID O6GMW1;
AC O6GMW1;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stampstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
RA Krzyviński M.I., Skaleka U., Smalhe D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL:BC073791; AAH73791.1; -.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG-1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-sect; 1.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG1; 1.
DR SMART: SM00406; IG1; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.
DR PROSITE: PS00230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFAC437 CRC64;
Query Match 77.1%; Score 439; DB 2; Length 236;
Best Local Similarity 81.3%; Pred. No. 5.2e-38;
Matches 87; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 2 IQMTQSSSLASVGVDRVTITCSASQDISNYLWYQKPKAVKLLIFYSSNLHSGVPSR 61
DB 24 IQMTQSSSLASVGVDRVTITCSASQDISNYLWYQKPKAVKLLIFYSSNLHSGVPSR 83
QY 62 FSGGSGGTDYTLTISLQPEDIAATYFCHQYSKLPWTFGGTKEIKR 108
DB 84 FSGGSGGTDYTLTISLQPEDIAATYFCHQYSKLPWTFGGTKEIKR 130
RESULT 15
KVLP_HUMAN STANDARD; PRT; 108 AA.
ID KVLP_HUMAN
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-1 region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barikol H.U., Hess M., Langer B., Ponstingl H.,
RA Seimetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press, New
York (1969).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Framework-2.
FT DOMAIN 35 49 Framework-3.
FT DOMAIN 50 56 Framework-4.
FT DOMAIN 57 88 Framework-5.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISUPID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACED5A313DF3A CRC64;
Query Match 77.1%; Score 438; DB 1; Length 108;
Best Local Similarity 78.7%; Pred. No. 2.6e-38;
Matches 85; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
QY 1 DIQMTQSSSLASVGVDRVTITCSASQDISNYLWYQKPKAVKLLIFYSSNLHSGVPS 60
DB 1 DIQMTQSSSLASVGVDRVTITCSASQDISNYLWYQKPKAVKLLIFYSSNLHSGVPS 60
QY 61 FSGGSGGTDYTLTISLQPEDIAATYFCHQYSKLPWTFGGTKEIKR 108
DB 61 FSGGSGGTDYTLTISLQPEDIAATYFCHQYSKLPWTFGGTKEIKR 130
Search completed: December 23, 2004, 19:04:38
Job time : 31.044 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04; Search time 31.8339 Seconds

(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624
Sequence: 1 EVTLVSGDFVKGSLKV.....KLGTYVDSMGQSTTLVSS 119

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

A_GeneSeq_23Sep04:.*
1: geneseqp1980s:.*
2: geneseqp1980s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	119	4 AAB81989	Aab81989 Ganglioside
2	624	100.0	119	6 ABU11012	ABU11012 Modified
3	624	100.0	130	2 AAR33256	Aar33256 Rat Immun
4	624	100.0	130	2 AAR53341	Aar53341 KM641 L C
5	624	100.0	130	2 AAY28369	Aay28369 PKM641 HA
6	624	100.0	130	3 AAB01627	Aab01627 Murine im
7	624	100.0	138	4 AAB81977	Aab81977 Ganglioside
8	624	100.0	138	6 ABU11002	ABU11002 Modified
9	624	100.0	582	4 AAB81991	Aab81991 Ganglioside
10	579	92.8	119	4 AAB81985	Aab81985 Ganglioside
11	579	92.8	119	6 ABU11010	ABU11010 Modified
12	579	92.8	582	4 AAB81987	Aab81987 Ganglioside
13	493	79.0	119	2 AAW29994	Aaw29994 Heavy cha
14	487	78.0	134	6 ABP60555	ABP60555 Murine an
15	486.5	78.0	294	4 AAB20442	Aab20442 Anti-FIX/
16	486.5	78.0	325	4 AAB20438	Aab20438 Anti-FIX/
17	486.5	78.0	732	4 AAB20437	Aab20437 Anti-FIX/
18	486	77.9	140	6 ABG74241	ABG74241 Mouse ant
19	485	77.9	247	4 AAB20436	Aab20436 Anti-FIX/
20	482.5	77.3	249	4 AAB20435	Aab20435 Anti-FIX/
21	481	77.1	121	5 AAE16426	AAE16426 Mouse ant
22	480.5	76.9	121	6 ABR41818	ABr41818 Heavy cha
23	480	76.9	119	6 AAW29996	Aaw29996 Humanised
24	480	76.9	237	7 AAE38657	AAE38657 Mouse GI
25	477.5	76.5	121	8 ADM78071	Adm78071 Human SKB

ALIGNMENTS

26	477	76.4	232	7	ADP72730	Adf72730 Divalent
27	477	76.4	241	7	ADP72729	Adf72729 Monovalen
28	477	76.4	255	7	ADP72734	Adf72734 His-tagge
29	475.5	76.2	249	4	AAB20435	Aab20435 Anti-FIX/
30	475	76.1	119	5	AAU72814	Aau72814 Humanised
31	475	76.1	119	6	AAO29882	Aao29882 M-type fu
32	475	76.1	119	7	ADJ79825	Adj79825 M-type fu
33	475	76.1	249	4	AAB20434	Aab20434 Anti-FIX/
34	475	76.1	462	6	AAO29869	Aao29869 Mouse ant
35	475	76.1	462	7	ADJ79787	Adj79787 TRA-8 ant
36	475	76.1	464	5	AAU72801	Aau72801 TRA-8 hea
37	473.5	75.9	120	5	AAO18391	Aao18391 Murine CB
38	472	75.6	119	2	AA879887	Aar79887 Anti-EGFR
39	472	75.6	239	2	AA879866	Aar79866 Anti-EGFR
40	471	75.5	262	6	ABR42295	ABr42295 Bispecifi
41	471	75.5	262	6	ABR42293	ABr42293 Bispecifi
42	471	75.5	262	6	ABR42290	ABr42290 Diabody h
43	471	75.5	268	6	ABR42291	ABr42291 Bispecifi
44	471	75.5	268	6	ABR42288	ABr42288 Diabody 6
45	471	75.5	268	6	ABR42287	ABr42287 Diabody 6

RESULT 1
AAB81989
ID AAB81989 standard; protein; 119 AA.

AC AAB81989;

DT 03-JUL-2001 (first entry)

DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 55.

KM Ganglioside; GD3; complementarily determining region; CDR; antibody;

KW cancer.

OS Mus musculus.

PN W0200123432-A1.

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP06774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105086.

QY 1 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 60
 DB 1 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 60
 QY 61 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 119
 DB 61 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 119

RESULT 2

ABU1012 standard; protein; 119 AA.

AC ABU1012;

DT 04-FEB-2003 (first entry)

DE Modified ganglioside GD3 antibody associated protein #5.

KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.

OS Mus musculus.

PN WO200278739-A1.

PD 10-OCT-2002.

PF 29-MAR-2002; 2002WO-JP003170.

PR 29-MAR-2001; 2001JP-00097483.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Shitara K, Niwa R, Kanazawa J, Asada M;

DR WPI; 2003-067410/06.

PT Drugs containing genetically-modified antibody against ganglioside GD3, its fragment, immunocompetent cell activators or/and anticancer agents in combination, applicable in treating malignant tumor like melanoma.

PS Claim 7; Page 112-113; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumour CC like melanoma and can provide a treatment with enhanced therapeutic CC effect and little side-reactions, particularly to relieve problems of CC side-effects during the conventional single administration. This sequence CC represents a protein associated with the anti- ganglioside GD3 antibody

XX Sequence 119 AA;

Query Match 100.0%; Score 624; DB 6; Length 119;
 Best Local Similarity 100.0%; Pred. No. 7, 4e-51;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 60
 DB 1 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 60
 QY 61 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 119
 DB 61 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 119

RESULT 3

AAR33256 standard; protein; 130 AA.

AC AAR33256;

XX 25-MAR-2003 (revised)
 DT 12-JUL-1993 (first entry)

DE Rat immunoglobulin H chain variable region of pKM641HA3.

KM Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
 KW humanised; chimeric; antibody; expression vector.

XX Rattus rattus.

OS Key Location/Qualifiers

FT Peptide 1..10

FT Protein /note= "Signal peptide"

FT /note= "Mature protein"

PN EP53199-A2.

PD 24-MAR-1993.

PF 18-SEP-1992; 92EP-00116026.

PR 18-SEP-1991; 91JP-00238375.

XX (KYOW) KYOWA HAKKO KOGYO CO LTD.

PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

DR WPI; 1993-095510/12.

PT Humanised chimeric antibody produ. against ganglioside GD3 - for treating

PS Claim 6; Page 29-30; 63pp; English.

CC The sequences given in AAR33256-57 represent rat heavy and light chain CC variable regions respectively. The DNA sequences encoding these proteins CC were used in the construction of humanised chimeric antibody expression CC vectors. In these humanised antibodies none of the amino acids of the non CC -human animal Ab variable region have been changed. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 130 AA;

Query Match 100.0%; Score 624; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 8, 2e-51;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 60
 DB 11 EYTLVESGGDFYKPGGSLKVSQASGFAFSHYAMSVWROTPAKRLEWVAIYSSGSGTYY 70
 QY 61 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 119
 DB 71 SDSVKGRTFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTYYPDSWGCGTTTLTVSS 129

RESULT 4

AAR53341 standard; protein; 130 AA.

AC AAR53341;

DT 18-NOV-1994 (first entry)

DE KM641 L chain variable region.

KM Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
 KW expression vector; heavy; light; chain; hypervariable region; CDR;
 XX constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.


```

OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
XX /label= sig_peptide
XX
XX AU9346181-A.
XX
XX 17-MAR-1994.
XX
XX
XX 07-SEP-1993; 93AU-00046181.
XX
XX 07-SEP-1992; 92JP-00238452.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M,
XX WPI; 1994-126857/16.
XX DR N-PSDB; AAQ63439.
XX
XX
XX Humanised antibody specific for ganglioside GM2 - used for producing a
XX PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.
XX
XX
XX Example 2; Page 116-117; 191pp; English.
XX
XX
XX Example 2 describes the construction of the vector pchic41HA3 for
XX CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
XX CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
XX CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
XX CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
XX CC AA045438-39. A KM641-derived chimeric human Ab H chain expression vector
XX CC was constructed by joining the H chain variable region gene from
XX CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
XX CC synthetic DNAs given in AAQ63439 and AAQ63440
XX
XX
XX Sequence 130 AA:
SQ
Query Match 100.0%; Score 624; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.2e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGDFVPRGSLKYSKASGFAFSGHYMSWVROTPARLEWVAIYSSGSGSTYY 60
DB 11 EVTLVESGDFVPRGSLKYSKASGFAFSGHYMSWVROTPARLEWVAIYSSGSGSTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSEDSAMVFCTRVKLGTYYPDSWCGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLSRSEDSAMVFCTRVKLGTYYPDSWCGTTLTVSS 129
XX
XX
XX RESULT 5
XX AA28369
XX ID AAY28369 standard; protein; 130 AA.
XX
XX
XX AAY28369;
XX
XX
XX 04-NOV-1999 (first entry)
XX
XX
XX pKM641 HA3 immunoglobulin heavy chain.
XX
XX
XX antibody; nucleotide; genomic; hypervariable region; chimeric;
XX KM light chain; amino acid.
XX
XX
XX Mus sp.
XX OS
XX US939532-A.
XX PN
XX 17-AUG-1999.
XX PD
XX 07-JUN-1995; 95US-00483528.
XX PF
XX 07-SEP-1993; 93US-00116778.
XX PR

```

```

XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K,
XX PI
XX WPI; 1999-468416/39.
XX DR
XX DR N-PSDB; AAX99482.
XX
XX
XX Chimeric human antibody expression vectors.
XX
XX
XX Example 1; Col 99-101; 188pp; English.
XX
XX
XX This immunoglobulin region was isolated from pKM641HA3. This sequence has
XX CC no methionine initiation codon and the leader sequence was partly
XX CC lacking. The chimeric human antibodies are useful in the treatment of
XX CC cancer, especially that which is of neural ectodermal origin. In contrast
XX CC to prior art constructs based on mouse monoclonal antibodies, the
XX CC chimeric human antibodies do not cause anti-mouse immunoglobulin
XX CC production. The chimeric human antibodies have a prolonged half-life and
XX CC a reduced frequency of adverse effects when compared to mouse monoclonal
XX CC antibodies
XX
XX
XX Sequence 130 AA:
SQ
Query Match 100.0%; Score 624; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.2e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGDFVPRGSLKYSKASGFAFSGHYMSWVROTPARLEWVAIYSSGSGSTYY 60
DB 11 EVTLVESGDFVPRGSLKYSKASGFAFSGHYMSWVROTPARLEWVAIYSSGSGSTYY 70
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSEDSAMVFCTRVKLGTYYPDSWCGTTLTVSS 119
DB 71 SDSVKGRFTISRDNKNTLYLQWRSLSRSEDSAMVFCTRVKLGTYYPDSWCGTTLTVSS 129
XX
XX
XX RESULT 6
XX AAB01627
XX ID AAB01627 standard; protein; 130 AA.
XX
XX
XX AAB01627;
XX
XX
XX 07-DEC-2000 (first entry)
XX
XX
XX Murine immunoglobulin heavy chain variable region.
XX
XX
XX Mouse; immunoglobulin, H chain; heavy chain; variable region; cancer;
XX KM humanised antibody.
XX
XX
XX Mus sp.
XX OS
XX
XX Key Location/Qualifiers
XX FH 1..10
XX FT Peptide /label= signal_peptide
XX FT Protein 11..130
XX /label= mature_immunoglobulin_heavy_chain_variable_region
XX
XX
XX EP1013761-A2.
XX PN
XX
XX 28-JUN-2000.
XX PD
XX 18-SEP-1992; 99EP-00124345.
XX PF
XX 18-SEP-1991; 91JP-00238375.
XX PR
XX 18-SEP-1992; 92EP-00116026.
XX
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX PA
XX Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;
XX PI
XX WPI; 2000-402204/35.
XX DR
XX N-PSDB; AAA51003.

```

XX New humanized chimera antibody KM-871 useful for treating cancer,
PT comprises variable region of mouse monoclonal antibody, reactive with
PT ganglioside and human antibody constant region.
PS Claim 14; Page 27-28; 65pp; English.
XX
XX The present sequence is a murine immunoglobulin heavy chain variable
CC region from plasmid KM-641. The coding sequence was used in the creation
CC of an expression vector, along with the sequence for a human antibody, to
CC produce humanised chimaeric antibodies, which can be used to treat
CC cancer. Humanised chimaeric antibodies are more effective than mouse
CC antibodies as they do not provoke a reaction in the human and side
CC effects, such as the formation of anti-mouse immunoglobulin antibody and
CC the rapid half-life of the immunoglobulins, do not occur
XX
SQ Sequence 130 AA;
XX
Query Match 100.0%; Score 624; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.2e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 60
DB 11 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 70
QY 61 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 119
DB 71 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 129
RESULT 7
AAB81977
ID AAB81977 standard; protein; 138 AA.
XX
XX AAB81977;
XX
XX 03-JUL-2001 (first entry)
XX
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 1.
XX
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.
XX
XX Mus musculus.
XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000MO-JP006774.
XX
XX 30-SEP-1999; 99JP-00278291.
XX
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Shitara K, Nakamura K, Niwa R;
XX
XX WPI; 2001-266143/27.
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Example 1; Page 138-139; 183pp; Japanese.
XX
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention

XX
SQ Sequence 138 AA;
XX
Query Match 100.0%; Score 624; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.7e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 60
DB 20 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 79
QY 61 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 119
DB 80 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 138
RESULT 8
ABU11002
ID ABU11002 standard; protein; 138 AA.
XX
XX ABU11002;
XX
XX 04-FEB-2003 (first entry)
XX
XX Modified ganglioside GD3 antibody associated protein #1.
XX
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
XX
XX Mus musculus.
XX
XX WO200278739-A1.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-JP003170.
XX
XX 29-MAR-2001; 2001JP-00097483.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Shitara K, Niwa R, Kanazawa J, Asada M;
XX
XX WPI; 2003-067410/06.
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT its fragment, immunocompetent cell activators or/and antitumor agents in
PT combination, applicable in treating malignant tumor like melanoma.
XX
XX Example 3; Page 97; 121pp; Japanese.
XX
XX The invention describes drugs contain a genetically-modified antibody
CC against ganglioside GD3 or its fragment and at least 1 of a substance
CC capable of activating immunocompetent cells and a substance having an
CC anticancer activity in combination. The drugs can be used to treat tumour
CC like melanoma and can provide a treatment with enhanced therapeutic
CC effect and little side-reactions, particularly to relieve problems of
CC side-effects during the conventional single administration. This sequence
CC represents a protein associated with the anti- ganglioside GD3 antibody
XX
SQ Sequence 138 AA;
XX
Query Match 100.0%; Score 624; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.7e-51;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 60
DB 20 EYTLVSSGGDFPVKPGGSLKVCASGFAFSHYAMSWVROTAPAKRLFWAVYISSGSGTTY 79
QY 61 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 119
DB 80 SDSVKGRTTISRDNANKNTLYLQWRSLSRSDSAMVFCRTVKLGTYYPDSWGQGTTLTVSS 138

RESULT 9
AAB81991 standard; protein; 582 AA.
ID AAB81991 standard; protein; 582 AA.
AC AAB81991;
XX
XX 03-JUL-2001 (first entry)
DT
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.
XX
XX Synthetic.
OS
XX WO200123432-A1.
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000MO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 39; Page 175-179; 183pp; Japanese.
PS
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
Query Match 100.0%; Score 624; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.2e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVTLVESGDFVPRGSLKYSKASGAFSHYAMSWVRQTPAKRLEWVAVYISSGSGSTYY 60
XX
XX 1 EVTLVESGDFVPRGSLKYSKASGAFSHYAMSWVRQTPAKRLEWVAVYISSGSGSTYY 60
DB
QY 61 SDSVKGRFTISRDNANKTLYLQKRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTLLTVSS 119
XX
XX 61 SDSVKGRFTISRDNANKTLYLQKRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTLLTVSS 119
DB
RESULT 10
AAB81985 standard; protein; 119 AA.
ID AAB81985 standard; protein; 119 AA.
AC AAB81985;
XX
XX 03-JUL-2001 (first entry)
DT
XX Ganglioside GD3 specific antibody related protein SEQ ID NO: 9.
DE
XX Ganglioside; GD3; complementarity determining region; CDR; antibody;
KM cancer.
XX
XX Synthetic.

XX
XX WO200123432-A1.
XX
XX 05-APR-2001.
PD
XX
XX 29-SEP-2000; 2000MO-JP006774.
PF
XX 30-SEP-1999; 99JP-00278291.
PR
XX 06-APR-2000; 2000JP-00105088.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Hanai N, Shitara K, Nakamura K, Niwa R;
PI
XX WPI; 2001-266143/27.
DR
XX
XX New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
XX Claim 20; Page 142-143; 183pp; Japanese.
PS
XX The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumors, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 119 AA;
Query Match 92.8%; Score 579; DB 4; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.2e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EVTLVESGDFVPRGSLKYSKASGAFSHYAMSWVRQTPAKRLEWVAVYISSGSGSTYY 60
XX
XX 1 EVTLVESGDFVPRGSLKYSKASGAFSHYAMSWVRQTPAKRLEWVAVYISSGSGSTYY 60
DB
QY 61 SDSVKGRFTISRDNANKTLYLQKRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTLLTVSS 119
XX
XX 61 SDSVKGRFTISRDNANKTLYLQKRSLSRSDSAMYFCTRVKLGTYYPDSWGQGTLLTVSS 119
DB
RESULT 11
ABU11010 standard; protein; 119 AA.
ID ABU11010 standard; protein; 119 AA.
AC ABU11010;
XX
XX 04-FEB-2003 (first entry)
DT
XX
XX Modified ganglioside GD3 antibody associated protein #3.
DE
XX Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
KM
XX
XX Synthetic.
OS
XX WO200278739-A1.
XX
XX 10-OCT-2002.
PD
XX 29-MAR-2002; 2002MO-JP003170.
PF
XX 29-MAR-2001; 2001JP-00097483.
PR
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Shitara K, Niwa R, Kanazawa J, Asada M;
PI
XX WPI; 2003-067410/06.
DR
XX
XX Drugs containing genetically-modified antibody against ganglioside GD3,
PT

its fragment, immunocompetent cell activators or/and anticancer agents in combination, applicable in treating malignant tumor like melanoma.

PS Claim 8; Page 99; 121pp; Japanese.

CC The invention describes drugs contain a genetically-modified antibody against ganglioside GD3 or its fragment and at least 1 of a substance capable of activating immunocompetent cells and a substance having an antitumor activity in combination. The drugs can be used to treat tumor like melanoma and can provide a treatment with enhanced therapeutic effect and little side-effects, particularly to relieve problems of side-effects during the conventional single administration. This sequence represents a protein associated with the anti- ganglioside GD3 antibody

XX

SQ Sequence 119 AA;

Query Match 92.8%; Score 579; DB 6; Length 119;
Best Local Similarity 91.6%; Pred. No. 1.2e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVYKPGGSLKVCASGPAFASHYAMSVWROTAPKRLIEWAVYISGSGSGTYY 60
DB 1 EVQLVESGGDFVQPGGSLKLVSCAASGPAFASHYAMSVWROAPKGLIEWAVYISGSGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYVKGITYYFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYVKGITYYFDSWGQGTLLTVSS 119

RESULT 12

AAB81987 standard; protein; 582 AA.

AC AAB81987;
XX
DT 03-JUL-2001 (first entry)
XX
DB Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX cancer.

OS Synthetic.
XX
PN MO200123432-A1.
XX

PD 05-APR-2001.

PF 29-SEP-2000; 2000WO-JP006774.

PR 30-SEP-1999; 99JP-00278291.

PR 06-APR-2000; 2000JP-00105088.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Hanai N, Shitara K, Nakamura K, Niwa R;

PI MPI; 2001-266143/27.

XX New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent activity in cancer.

PS Claim 41; Page 168-172; 183pp; Japanese.

CC The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumors, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention

CC

XX Sequence 582 AA;

Query Match 92.8%; Score 579; DB 4; Length 582;
Best Local Similarity 91.6%; Pred. No. 7e-46;
Matches 109; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVYKPGGSLKVCASGPAFASHYAMSVWROTAPKRLIEWAVYISGSGSGTYY 60
DB 1 EVQLVESGGDFVQPGGSLKLVSCAASGPAFASHYAMSVWROAPKGLIEWAVYISGSGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYVKGITYYFDSWGQGTLLTVSS 119
DB 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYVKGITYYFDSWGQGTLLTVSS 119

RESULT 13

AAW29994 standard; protein; 119 AA.

AAW29994;

DT 25-MAR-2003 (revised)
XX
DT 12-MAR-1998 (first entry)
XX

DE Heavy chain variable region of MAb for t1A.

KM Heavy chain; variable region; monoclonal antibody; human; CD6; murine;
XX Leucocyte differentiation antigen; hybridoma; humanisation; mutagenesis;
XX PCR; primer; amplification; inflammatory infiltration; skin; psoriasis;
XX diagnosis.

XX Mus sp.

PN MO9719111-A2.

PD 29-MAY-1997.

PF 18-NOV-1996; 96WO-CU000004.

PR 17-NOV-1995; 95CU-00000120.

PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.

PI Montero Casimiro JE, Lombardero Valladares J, Perez Rodriguez R;
XX Sierra Blazquez P, Tormo Bravo BR;

DR MPI; 1997-298060/27.

PT Monoclonal antibody against human CD6 antigen - useful for diagnosis and treatment of psoriasis.

PS Claim 3; Page 27; 38pp; Spanish.

CC This is the amino acid sequence of the heavy chain variable region of the monoclonal antibody (Mab) for t1A which recognises the human leucocyte differentiation antigen CD6. The Mab is a murine IgG2-type Ab produced by the usual hybridoma techniques. The coding sequence for the variable CC region can be used to generate humanised variants, especially by CC mutagenic PCR. CD6 has been shown to be expressed in T lymphocytes CC involved in the inflammatory infiltration of the skin in psoriasis. The CC anti-CD6 Mab can therefore be used to diagnose and treat psoriasis. CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 119 AA;

Query Match 79.0%; Score 493; DB 2; Length 119;
Best Local Similarity 81.5%; Pred. No. 1.5e-38;
Matches 97; Conservative 3; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVTLVESGGDFVYKPGGSLKVCASGPAFASHYAMSVWROTAPKRLIEWAVYISGSGSGTYY 60
DB 1 EVQLVESGGGLVQPGGSLKLVSCAASGPAFASHYAMSVWROAPKGLIEWAVYISGSGSGTYY 60
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYVKGITYYFDSWGQGTLLTVSS 119

Db 61 PDSVKGKFTISRDNKNTLYLQWSSLSKSEPTAMYYCARPDYDLVFPDSMGCTTLTVSS 119

RESULT 14

ID ABB60555 standard; protein; 134 AA.

XX ABB60555;

DT 21-MAR-2003 (first entry)

DE Murine antibody 14F3 heavy chain variable region.

XX Mouse; monoclonal antibody; 14F3; osteopathic; antirheumatic;
 KM antiarthritic; antiinflammatory; cytostatic; antipsoriatic; antidiabetic;
 KM neuroprotective; gene therapy; rheumatoid arthritis; osteoporosis;
 KM bone cancer; osteolysis; osteoarthritis; immune disease; psoriasis;
 KM insulin-dependent diabetes; inflammatory bowel disease;
 KM multiple sclerosis; heavy chain variable region;
 KM complementary determining region; CDR.

XX Mus musculus.

OS Key Location/Qualifiers

FT Region 31..35

FT Region /label= CDR1

FT Region 50..56

FT Region /label= CDR2

FT Region 99..110

FT Region /label= CDR3

XX MO200295012-A1.

PD 28-NOV-2002:

XX 03-MAY-2002; 2002MO-US014246.

XX 18-MAY-2001; 2001US-0292031P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Sweet RW, Tornetta MA, Watram TA;

PI WPI; 2003-156758/15.

DR N-PSDB; ABBV99887.

XX New monoclonal antibody having the characteristics of a monoclonal

PT antibody 14F3, useful for treating or preventing osteopathic diseases,

PT e.g. rheumatoid arthritis, or osteoporosis, and immune diseases e.g.

PT psoriasis, or diabetes.

XX Disclosure; Page 8; 51P; English.

XX The invention relates to a novel monoclonal antibody having the

CC identifying characteristics of, or that is a monoclonal antibody 14F3. An

CC antibody of the invention has osteopathic, antirheumatic, antidiabetic,

CC antiinflammatory, cytostatic, antipsoriatic, antidiabetic, and

CC neuroprotective activity. The polynucleotides encoding the antibodies of

CC the invention may have a use in gene therapy. The antibodies and

CC polypeptides are useful for treating or preventing osteopathic diseases,

CC such as rheumatoid arthritis, osteoporosis, metastatic, and primary bone

CC cancer, wear debris induced osteolysis or osteoarthritis, and immune

CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory

CC bowel disease or multiple sclerosis. The present sequence represents the

CC heavy chain variable region of the murine monoclonal antibody 14F3 of the

CC invention. The sequence contains three complementary determining regions

CC (CDR's)

XX Sequence 134 AA;

XX Query Match

78.0%; Score 487; DB 6; Length 134;

Best Local Similarity 79.3%; Pred. No. 6e-38; Matches 96; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVTLVSGGDPFKVPGGSLKVSCAASGFAFSHYAMSVRQTPAKRLKLVAVYISGGSGTTY 60

Db 1 EVTLVSGGDLVPRGSLKVSCAASGTFGRYGMVWRQTPDKRLKLVAVYISGGSGTTY 60

QY 61 SDSVKGKFTISRDNKNTLYLQWSSLSKSEPTAMYYCARPDYDLVFPDSMGCTTLTVSS 118

Db 61 PDSVKGKFTISRDNKNTLYLQWSSLSKSEPTAMYYCARPDYDLVFPDSMGCTTLTVSS 120

QY 119 S 119

Db 121 S 121

RESULT 15

ID AAB20442 standard; protein; 294 AA.

XX AAB20442;

AC AAB20442;

DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 198/BI-myc-tag fusion.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;

KM Factor VIII cofactor; blood coagulation disorder; haemophilia A;

KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.

XX Mus musculus.

OS Synthetic.

OS Escherichia coli.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..22

FT Peptide /label= Signal_peptide

FT Protein 23..294

FT Protein /label= Mature_protein

FT Protein 23..271

FT Region /label= scFv

FT Region 23..144

FT Misc-difference 76

FT Peptide /note= "encoded by GGN"

FT Peptide 145..159

FT Region /label= Linker

FT Peptide 160..271

FT Peptide /label= VL

FT Protein 272..274

FT Protein /label= Spacer

FT Peptide 275..286

FT Peptide /label= Myc_tag

FT Peptide 287..288

FT Peptide /label= Spacer

FT Peptide 289..294

FT Peptide /label= His_tag

XX MO200119992-A2.

PD 22-MAR-2001.

XX 13-SEP-2000; 2000MO-EP008936.

XX 14-SEP-1999; 99AT-00001576.

XX (BAXT) BAXTER AG.

PI Schellfänger F, Kerschbaumer R, Falkner F, Dörner F,

XX WPI; 2001-290358/30.

DR N-PSDB; AAF30732.

XX New factor IX/factor IXa antibodies and their derivatives useful for
 PR increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
 XX

PS Example 18; Fig 34; 138pp; English.

XX
 CC The present sequence is that of a fusion protein comprising: a PelB
 CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
 CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
 CC an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
 CC spacer; and a C-terminal 6His affinity tail. 198/B1 is an example of anti-
 CC -human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
 CC invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv
 CC fragments, have FVIII cofactor activity or FIXa activating activity.
 CC Administration leads to an increase in the procoagulant activity of FIXa,
 CC even in the presence of FVIII inhibitors. This allows for rapid blood
 CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
 CC FVIII inhibitor patients. The antibodies and derivatives are used in a
 CC claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It exhibited
 CC FVIII-like activity
 CC

XX Sequence 294 AA;

Query Match 78.0%; Score 486.5; DB 4; Length 294;

Best Local Similarity 78.7%; Pred. No. 1.6e-37; Indels 3; Gaps 1;

Matches 96; Conservative 6; Mismatches 17; Indels 3; Gaps 1;

QY	1	EVTLVESG	60
			60
DB	23	EYKLVESGGGLVKGPGSLKSCAASGFTSSYTM	82
			82
QY	61	SDSVKGRFTISRDNKNTLYLQMRSLRSDSAMYFCTRYKLG--	117
			117
DB	83	PDSVKGRFTISRDNKNTLYLQMSLRSDTAMYCTREGGFTVMYFDPVWGAGTSTVTV	142
			142
QY	118	SS 119	
DB	143	SS 144	

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 Job time : 33.8339 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 / Search time 7.85924 Seconds
(without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624

Sequence: 1 EVTLVSGGDFVKGSLKV.....KLGTYRDSMGQGTTLVSS 119

Scoring table:

BLOSUM62

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/6C COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624	100.0	130	4 US-09-225-322B-18	Sequence 18, Appl
2	624	100.0	130	4 US-09-764-304-18	Sequence 18, Appl
3	614	98.4	130	4 US-09-225-322B-8	Sequence 8, Appl
4	614	98.4	130	4 US-09-764-304-8	Sequence 8, Appl
5	493	79.0	119	4 US-08-875-674A-1	Sequence 1, Appl
6	486	77.9	247	5 PCT-US94-07659-2	Sequence 2, Appl
7	480	76.9	119	4 US-08-875-674A-3	Sequence 3, Appl
8	472	75.6	239	2 US-08-553-497A-18	Sequence 18, Appl
9	469.5	75.2	135	3 US-08-579-378A-16	Sequence 16, Appl
10	466.5	74.8	118	1 US-08-326-362-2	Sequence 2, Appl
11	464	74.4	119	3 US-09-406-535-2	Sequence 2, Appl
12	460.5	73.8	124	4 US-09-518-737-2	Sequence 2, Appl
13	457.5	73.3	456	4 US-09-495-880A-11	Sequence 11, Appl
14	457	73.2	217	5 PCT-US94-14106-59	Sequence 59, Appl
15	453	72.6	119	4 US-09-648-067A-15	Sequence 15, Appl
16	452	72.4	119	1 US-08-497-312-20	Sequence 20, Appl
17	450.5	72.2	120	2 US-07-934-373C-4	Sequence 4, Appl
18	450.5	72.2	120	3 US-08-437-642B-4	Sequence 4, Appl
19	450.5	72.2	120	4 US-08-146-206C-4	Sequence 4, Appl
20	450.5	72.2	120	4 US-09-705-686-4	Sequence 4, Appl
21	450.5	72.2	130	4 US-09-705-392A-4	Sequence 4, Appl
22	450	72.1	119	2 US-08-475-000-16	Sequence 16, Appl
23	450	72.1	119	2 US-08-483-199-16	Sequence 16, Appl
24	450	72.1	119	2 US-08-484-508-16	Sequence 16, Appl
25	449.5	72.0	123	1 US-08-356-272-3	Sequence 3, Appl
26	449	72.0	121	1 US-08-339-582-2	Sequence 2, Appl
27	448.5	71.9	135	3 US-08-579-378A-20	Sequence 20, Appl

28	448.5	71.9	443	5 PCT-US96-13152-4	Sequence 4, Appl
29	447	71.6	119	1 US-08-331-398A-46	Sequence 46, Appl
30	447	71.6	119	2 US-08-331-397B-46	Sequence 46, Appl
31	447	71.6	119	2 US-08-759-804A-46	Sequence 46, Appl
32	447	71.6	119	3 US-09-227-693-46	Sequence 46, Appl
33	447	71.6	123	3 US-09-344-587-13	Sequence 13, Appl
34	445.5	71.4	167	4 US-09-318-786-31	Sequence 31, Appl
35	445	71.3	117	3 US-08-752-693A-3	Sequence 3, Appl
36	445	71.3	126	3 US-08-976-183A-31	Sequence 31, Appl
37	445	71.3	126	3 US-08-976-183A-32	Sequence 32, Appl
38	445	71.3	136	3 US-08-976-183A-33	Sequence 33, Appl
39	445	71.3	136	3 US-08-976-183A-34	Sequence 34, Appl
40	445	71.3	245	3 US-09-069-821-5	Sequence 5, Appl
41	445	71.3	245	4 US-09-956-086-5	Sequence 5, Appl
42	445	71.3	245	4 US-09-956-087-5	Sequence 5, Appl
43	445	71.3	447	6 5455030-1	Sequence 5, Appl
44	444.5	71.2	247	6 5455030-9	Sequence 5, Appl
45	444	71.2	125	2 US-08-428-197-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-225-322B-18

; Sequence 18, Application US/09225322B

; Patent No. 6437098

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO

; APPLICANT: HASEGAWA, MAMORU

; APPLICANT: MIYABI, HIROMASA

; APPLICANT: KIMURA, YOSHIOHISA

; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY

; FILE REFERENCE: 249-101

; CURRENT APPLICATION NUMBER: US/09/225,322B

; CURRENT FILING DATE: 1999-01-05

; PRIOR APPLICATION NUMBER: US 08/454,680

; PRIOR FILING DATE: 1995-05-31

; PRIOR APPLICATION NUMBER: US 08/408,133

; PRIOR FILING DATE: 1995-03-21

; PRIOR APPLICATION NUMBER: US 08/292,178

; PRIOR FILING DATE: 1994-08-17

; PRIOR APPLICATION NUMBER: US07/947,674

; PRIOR FILING DATE: 1992-09-17

; PRIOR APPLICATION NUMBER: JP 3-238375

; PRIOR FILING DATE: 1991-09-18

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 130

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641

US-09-225-322B-18

Query Match 100.0%; Score 624; DB 4; Length 130;

Best Local Similarity 100.0%; Pred. No. 8.8e-60;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVTLVSGGDFVKGSLKVS CAASGFARSHYMSVNRQTPAKRLTWMVAIYSGSGTTY 60

DB 11 EVTLVSGGDFVKGSLKVS CAASGFARSHYMSVNRQTPAKRLTWMVAIYSGSGTTY 70

QY 61 SDVSKRFTISRDNAGTLYLQWRSLRSEDSAMVFCRTVYLGTYRDSMGQGTTLVSS 119

DB 71 SDVSKRFTISRDNAGTLYLQWRSLRSEDSAMVFCRTVYLGTYRDSMGQGTTLVSS 129

RESULT 2

US-09-764-304-18

; Sequence 16, Application US/09764304

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/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 18
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-18
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Query Match          100.0%; Score 624; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.8e-60;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 60
        |||
DB      11 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 70
        |||

QY      61 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 119
        |||
DB      71 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 129
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RESULT 3
US-09-225-322B-8
/ Sequence 8, Application US/09225322B
/ Patent No. 6437098
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/225,322B
/ CURRENT FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 8
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/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-8
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Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 60
        |||
DB      11 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 70
        |||

QY      61 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 119
        |||
DB      71 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 129
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RESULT 4
US-09-764-304-8
/ Sequence 8, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 8
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: CDNA KM-641
US-09-764-304-8
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Query Match          98.4%; Score 614; DB 4; Length 130;
Best Local Similarity 99.2%; Pred. No. 1.1e-58;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 60
        |||
DB      11 EYTLVSGGDFVYKPGGSLKVS CAASGFAFSHYAMSWVROTPAKRLMWAYISSGSGGTY 70
        |||

QY      61 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 119
        |||
DB      71 SDSVKGRTISRDNANKNTLYLQMRSLRSEDSAMVFCCTRYVKGTYFFDSWGQGTTLTVSS 129
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RESULT 5
US-08-875-674A-1
/ Sequence 1, Application US/08875674A
/ Patent No. 6572857
```



```

GENERAL INFORMATION:
APPLICANT: MONTERO CASIMIRO, J. E.
APPLICANT: LOMBARDEO VALLADARES, J.
APPLICANT: PEREZ RODRIGUEZ, R.
APPLICANT: SIERRA BLAZQUEZ, P.
APPLICANT: TOMO BRAVO, B. R.
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
STREET: One Chase Road
CITY: Scarsdale
STATE: New York
COUNTRY: U.S.A.
ZIP: 10583
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
COMPUTER: Compatible PC IBM (80486, 8 M Ram).
OPERATING SYSTEM: Windows 95.
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,674A
FILING DATE: 17-July-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CU96/00004
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
REFERENCE/DOCKET NUMBER: P-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 723-4300
TELEFAX: (914)-723-4301
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
MOLECULE TYPE: Protein
HYPOTHEetical: No
ANTI-SENSE: No
FRAGMENT TYPE: -N Terminal fragment.
ORIGINAL SOURCE:
ORGANISM: Mouse Balb/c
INDIVIDUAL ISOLATE: for CIA
TISSUE TYPE: Murine hybridoma
IMMEDIATE SOURCE:
CLONE: Sub-clone for CIA
FEATURES:
IDENTIFICATION METHOD: Experimental.
OTHER INFORMATION: Sequence corresponding to the variable region
Patent No. 6572857
OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing human
US-08-875-674A-1
Query Match 79.0%; Score 493; DB 4; Length 119;
Best Local Similarity 81.5%; Pred. No. 1e-45; Indels 0; Gaps 0;
Matches 97; Conservative 3; Mismatches 19;
Dy 61 SDSVKGRFTTIRDNANKNTLLYLQMSRLRSSEDSAMTFCTRVKLGTYYFDSSGGGTTITVSS 119
Db 61 PDsvkgrfttirDNvknktllylqmsrlrsedptamyyCARdydldyfdsmggggttlTVss 119
PCT-US94-07659-2

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1  ? Sequence 2 Application PC/TUS9407659
2  ? GENERAL INFORMATION:
3  ? APPLICANT: Young, Peter
4  ? APPLICANT: Groos, Mitchell
5  ? APPLICANT: Jonak, Zdenka L.
6  ? APPLICANT: Theisen, Timothy
7  ? APPLICANT: Hurle, Mark
8  ? APPLICANT: Jackson, Jeffrey R.
9  ? TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
10 ? TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
11 ? TITLE OF INVENTION: Disorders in Man
12 ? NUMBER OF SEQUENCES: 21
13 ? CORRESPONDENCE ADDRESS:
14 ? ADDRESSEE: SmithKline Beecham Corporation - Corp.
15 ? ADDRESSEE: Intellectual Property
16 ? STREET: 709 Swedeland Road
17 ? CITY: King of Prussia
18 ? STATE: PA
19 ? COUNTRY: USA
20 ? ZIP: 19406-2799
21 ? COMPUTER READABLE FORM:
22 ? MEDIUM TYPE: Floppy disk
23 ? COMPUTER: IBM PC compatible
24 ? OPERATING SYSTEM: PC-DOS/MS-DOS
25 ? SOFTWARE: Patent In Release #1.0, Version #1.25
26 ? CURRENT APPLICATION DATA:
27 ? APPLICATION NUMBER: PCT/US94/07659
28 ? FILING DATE:
29 ? CLASSIFICATION:
30 ? PRIOR APPLICATION DATA:
31 ? APPLICATION NUMBER: US 08/090,534
32 ? FILING DATE: 09-JUL-1993
33 ? ATTORNEY/AGENT INFORMATION:
34 ? NAME: Sutton, Jeffrey A.
35 ? REGISTRATION NUMBER: 34,028
36 ? REFERENCE/DOCKET NUMBER: P50171-1
37 ? TELECOMMUNICATION INFORMATION:
38 ? TELEPHONE: (610) 270-5024
39 ? TELEFAX: (610) 270-5090
40 ? INFORMATION FOR SEQ ID NO: 2:
41 ? SEQUENCE CHARACTERISTICS:
42 ? LENGTH: 247 amino acids
43 ? TYPE: amino acid
44 ? TOPOLOGY: linear
45 ? MOLECULE TYPE: protein
46 ? PCT-US94-07659-2
47
48 ? Query Match 77.9%; Score 486; DB 5; Length 247;
49 ? Bect Local Similarity 79.0%; Pred. No. 1,4e-44;
50 ? Matches 94; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
51
52 QY 1 EETLVSSGDFVPRGSLKLVSCAASGFAASHYAMSWVRQTPAKRLIEWAYIISGSGGTY 60
53 |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
54 Db 20 EYHIVSGGGLVPRGSLKLVSCAASGFAASHYAMSWVRQTPAKRLIEWAYIISGSGGTY 79
55
56 QY 61 SDSVKGRTTISRDNAKNTLYLQMSLRSSDSAMFYCTRYKLGTYIFDSKGGGTYITVSS 119
57 |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
58 Db 80 PDTYKGRFTTISRDNAKNTLYLQMSLRSSDSAMFYCTRYKLGTYIFDSKGGGTYITVSS 138
59
60 RESULT 7
61 US-08-875-674A-3
62 ? Sequence 3, Application US/08875674A
63 ? Patent No. 6572857
64 ? GENERAL INFORMATION:
65 ? APPLICANT: MONTERO CASIMIRO, J. E.
66 ? APPLICANT: LOMBARDO VALLADARES, J.
67 ? APPLICANT: P REZ RODR GUEZ, R.
68 ? APPLICANT: SIERRA EL ZQUEZ, P.
69 ? APPLICANT: TORO BRAVO, B. R.
70 ? TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
71 ? NUMBER OF SEQUENCES: 4
72 ? CORRESPONDENCE ADDRESS:
73

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1 ADDRESS: Lackenbach Siegel Marzullo Aronson & Greenspan, P.C.
2 STREET: One Chase Road
3 CITY: Scarsdale
4 STATE: New York
5 COUNTRY: U.S.A.
6 ZIP: 10583
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
10 COMPUTER: Compatible PC IBM (80486, 8 M Ram).
11 OPERATING SYSTEM: Windows 95.
12 SOFTWARE: Word Perfect 5.0 for Windows 95.
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/875,674A
16 FILING DATE: 17-July-1997
17 CLASSIFICATION: 530
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/CU96/00004
21 FILING DATE: 18-NOV-1996
22 ATTORNEY/AGENT INFORMATION:
23 NAME: HENRY A. MARZULLO, JR.
24 REGISTRATION NUMBER: 20,910
25 REFERENCE/DOCKET NUMBER: P-12
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (914) 723-4300
28 TELEFAX: (914) 723-4301
29
30 INFORMATION FOR SEQ ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 119 Amino acid residues.
33 TYPE: Amino acid.
34 STRANDEDNESS: Unknown.
35 TOPOLOGY: Unknown.
36 MOLECULE TYPE: Protein
37 HYPOTHEICAL: NO
38 ANTI-SENSE: NO
39 FRAGMENT TYPE: -N Terminal fragment.
40 ORIGINAL SOURCE:
41 TISSUE TYPE: Animal cells.
42 CELL LINE: NSO " Sp 2/0 " CHO
43 IMMEDIATE SOURCE:
44 CLONE: Sub-clone for c1A
45
46 FEATURE:
47 IDENTIFICATION METHOD: By similarity with known sequence.
48 OTHER INFORMATION: Sequence corresponding to the humanized
49 Patent No. 6572857
50 OTHER INFORMATION: variant of sub-clone for c1A recognising human CD6, particula
51 US-08-875-674A-3
52
53 Query Match 76.9%; Score 480; DB 4; Length 119;
54 Best Local Similarity 79.0%; Pred. No. 2,6e-44;
55 Matches 94; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
56
57 QY 1 EVTLVESGADPEVRKGGSLKTVSCAASGAFSHYAMSWRQRPAPKALEWVAAYISSGSGTTY 60
58 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
59 1 EVOLVEVGSGGLVVRKGGSLKTVSCAASGAFKFSRYAMSWRQAPGKLEWVAATISSGSGTTY 60
60
61 QY 61 SDSVYKGFRTISRDAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYPDSWGGTLLTVSS 119
62 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
63 Db 61 PDSVYKGFRTISRDAKNTLYLQMRSLRSEDSAMYFCTRVKLGTYYPDSWGGTLLTVSS 119
64
65 RESULT 8
66 US-08-553-497A-18
67 Sequence 18, Application US/08553497A
68 Patent No. 5844093
69
70 GENERAL INFORMATION:
71 APPLICANT: KETTLERBOROUGH, C. A.
72 APPLICANT: BENDIG, MARY M.
73 APPLICANT: ANSELL, KEITH H.
74 APPLICANT: GUSSOW, DETLEF
75 APPLICANT: ADAM, JAUME
76 APPLICANT: MITJANS, FRANESEC
77 APPLICANT: ROSELL, ELISABET

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1 APPLICANT: BLASCO, FRANCESC
2 APPLICANT: PILIATS, JAIME
3 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
4 TITLE OF INVENTION: ANTIBODIES
5 NUMBER OF SEQUENCES: 30
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
8 STREET: 2200 CLARENDON BLVD. SUITE 1400
9 CITY: ARLINGTON
10 STATE: VA
11 COUNTRY: US
12 ZIP: 22201
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent in Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/553,497A
20 FILING DATE: 17-NOV-1995
21 CLASSIFICATION: 530
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: WO PCT/EP95/00978
24 FILING DATE: 16-MAR-1995
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: EP 94104160.0
27 FILING DATE: 17-MAR-1994
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: EP 94118970.6
30 FILING DATE: 02-DEC-1994
31 ATTORNEY/AGENT INFORMATION:
32 NAME: HAMLET-KING, DIANA
33 REGISTRATION NUMBER: 33,302
34 REFERENCE/DOCKET NUMBER: MERCK 1726
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 703-243-6333
37 TELEFAX: 703-243-6410
38 INFORMATION FOR SEQ ID NO: 18:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 239 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43 MOLECULE TYPE: protein
44
45 US-08-553-497A-18
46
47 Query Match 75.6%; Score 472; DB 2; Length 239;
48 Best Local Similarity 77.3%; Pred. No. 4,4e-43;
49 Matches 92; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
50
51 QY 1 EVTVESGDPVVRPGSLKYSCLASGFAFESHYMSVTRCTPARLEWAVYISGGSGTTY 60
52 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 Db 1 EVKLQESGGLVVRPGSLKLSCLASGFTFSSYGSWVRCTPDRLRLSVATISSGAYIY 60
54
55 QY 61 SDSVKGFTISRDNARKTLYLQMRSLRSPDSAMYFCRTVYLGYYPDGSGCTTIVSS 119
56 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 Db 61 PDSVKGFTISRDNARKTLYLQMSLKSSEDTAMYCARLETGYALDYWGQGTIVVSS 119
58
59 RESULT 9
60 US-08-579-378A-16
61 Sequence 16, Application US/08579378A
62 Patent No. 6210671
63 GENERAL INFORMATION:
64 APPLICANT: Co, Man Sung
65 TITLE OF INVENTION: Humanized Antibodies Reactive with
66 TITLE OF INVENTION: I-Selectin
67 NUMBER OF SEQUENCES: 20
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Townsend and Townsend and Crew
70 STREET: One Market Plaza, Stewart Tower, Suite 2000
71 CITY: San Francisco
72 STATE: California
73 COUNTRY: USA

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; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114636.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-16

Query Match          75.2%; Score 469.5; DB 3; Length 135;
Best Local Similarity 79.8%; Pred. No. 4,1e-43;
Matches 95; Conservative 6; Mismatches 15; Indels 3; Gaps 2;

QY 1 EYLVESGGDFVPGSLKVS CAAGFAFSHYAMSWVROTPAKRLKLEWVAIYSSGSGSTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 EYLVESGGGLVPGSLKLA CAAGSGFTFTYMSWVROTPEKLEWVAISIGSG- TTY 78

QY 61 SDSVKRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 79 PDSVKRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 135

RESULT 10
US-08-326-362-2
; Sequence 2, Application US/08326362
; Patent No. 5730981
; GENERAL INFORMATION:
; APPLICANT: Bogslet, Klaus
; APPLICANT: Seeman, Gerhard
; APPLICANT: Dippold, Wolfgang
; TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
; TITLE OF INVENTION: Its Preparation and Use as a Tumortherapeutic Agent
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parbow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/326,362
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/032,863
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: DE P 42 08 795.3
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481-1276-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-326-362-2

Query Match          74.8%; Score 466.5; DB 1; Length 118;
Best Local Similarity 77.3%; Pred. No. 7,3e-43;
Matches 92; Conservative 7; Mismatches 19; Indels 1; Gaps 1;

QY 1 EYLVESGGDFVPGSLKVS CAAGFAFSHYAMSWVROTPAKRLKLEWVAIYSSGSGSTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QVLOQSGGGLVPGSLTSCAASRFTFTYMSWVROTPEKLEWVAIYSSGSGSTYY 60

QY 61 SDSVKRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RDSVKRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 118

RESULT 11
US-09-406-535-2
; Sequence 2, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: T1e2 Antagonist Antibodies
; FILE REFERENCE: P50844
; CURRENT APPLICATION NUMBER: US/09/406,535
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 60/102,100
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-406-535-2

Query Match          74.4%; Score 464; DB 3; Length 119;
Best Local Similarity 74.8%; Pred. No. 1,4e-42;
Matches 89; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 EYLVESGGDFVPGSLKVS CAAGFAFSHYAMSWVROTPAKRLKLEWVAIYSSGSGSTYY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EYLVESGGGLVPGSLKSCAAGFTSDYGMHVRQAPEKLEWVAIYSSGSGSTYY 60

QY 61 SDSVKRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADTVKGRFTISRDNANKTLYLQMSLRSEDSAMYFCTRYVKGTYYPDSWGQGTTLTVSS 119

```

RESULT 12
US-09-518-737-2
; Sequence 2, Application US/09518737
; Patent No. 6709833
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
; APPLICANT: SAITO, NAOKI
; TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3,4-DIPHOSPHATE
; FILE REFERENCE: 1965/49618
; CURRENT APPLICATION NUMBER: US/09/518,737
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 1999-250209
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-518-737-2

Query Match 73.8%; Score 460.5; DB 4; Length 124;
Best Local Similarity 74.8%; Pred. No. 3.4e-42;
Matches 92; Conservative 7; Mismatches 17; Indels 7; Gaps 2;

QY 1 EVTLVSGGDPFKPGSLKVCSCAAGFAFSHYAMSWROTAPKRLIEWAVYISSGSGTYY 60
1 EVQLVESGGDLVKPGSLKLCSCAAGFTFSYGMWVROTPEKRLIEWAVTISDGGTYY 60
DB 1 EVQLVESGGDLVKPGSLKLCSCAAGFTFSYGMWVROTPEKRLIEWAVTISDGGTYY 60

QY 61 SDSVKGRTTISRDNANKNTLYLQMRSLRSEDSAMYFCT---VKLTGYYPDSWGQTTLVSS 116
61 PDSVKGRTTISRDNANKNTLYLQMSLSKSDTAMTYCARQGVNVCIAV---WGQTLVT 117

DB 117 VSS 119
118 VSA 120

QY 117 VSS 119
118 VSA 120

RESULT 13
US-09-495-880A-11
; Sequence 11, Application US/09495880A
; Patent No. 6667150
; GENERAL INFORMATION:
; APPLICANT: RUDERT, FRITZ
; APPLICANT: GE, LIMING
; APPLICANT: ILAG, VIC
; TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
; TITLE OF INVENTION: (POLY)PEPTIDE COMPLEX
; FILE REFERENCE: MORPHO/9
; CURRENT APPLICATION NUMBER: US/09/495,880A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: PCT/EP98/04836
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: EP 97 11 3319.4
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-scFv (anti-
; OTHER INFORMATION: HAG)-gene fliis encoded by phage vector fflag1A (circular)
US-09-495-880A-11

Query Match 73.3%; Score 457.5; DB 4; Length 456;
Best Local Similarity 75.8%; Pred. No. 3.6e-41;
Matches 91; Conservative 8; Mismatches 20; Indels 1; Gaps 1;

QY 1 EVTLVSGGDPFKPGSLKVCSCAAGFAFSHYAMSWROTAPKRLIEWAVYISSGSGTYY 60
170 EVQLVESGGDLVKPGSLKLCSCAAGFTFSYGMWVROTPEKRLIEWAVTISDGGTYY 229
DB 170 EVQLVESGGDLVKPGSLKLCSCAAGFTFSYGMWVROTPEKRLIEWAVTISDGGTYY 229

QY 61 SDSVKGRTTISRDNANKNTLYLQMRSLRSEDSAMYFCT---RVKLGTYYFDSWGQTTLVSS 119
230 PDSVKGRTTISRDNANKNTLYLQMSLSKSDTAMTYCARREYDENGFAVWGQTTLVVSA 289

RESULT 14
PCT-US94-14106-59
; Sequence 59, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 217 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-59

Query Match 73.2%; Score 457; DB 5; Length 217;
Best Local Similarity 75.6%; Pred. No. 1.6e-41;
Matches 90; Conservative 8; Mismatches 17; Indels 4; Gaps 1;

QY 1 EVTLVSGGDPFKPGSLKVCSCAAGFAFSHYAMSWROTAPKRLIEWAVYISSGSGTYY 60
1 EVKLVESGGDLVKPGSLKLCSCAAGFTFSDIYMWVROTPEKRLIEWAVTISDGGTYY 60
DB 1 EVKLVESGGDLVKPGSLKLCSCAAGFTFSDIYMWVROTPEKRLIEWAVTISDGGTYY 60

QY 61 SDSVKGRTTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVKLTGYYPDSWGQTTLVSS 119
61 ADSVKGRTTISRDNANKNTLYLQMSLSKSDTAMTYCARDPL---YGSWGQTTLVSS 115

RESULT 15
US-09-648-067A-15
; Sequence 15, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P175R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 15
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VH consensus sequence
US-09-648-067A-15

Query Match 72.6%; Score 453; DB 4; Length 119;
Best Local Similarity 71.4%; Pred. No. 2.1e-41;

Matches 85; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

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Db	1	EVOLVESGGGLVOPGGSILRLSCAASGFTFSSYAMSWRQAPGKLEWVAIYSSGSGSTYY	60
Qy	61	SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFPDSWGQGTLLTVSS	119
Db	61	ADSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVKLGTYFPDSWGQGTLLTVSS	119

Search completed: December 23, 2004, 19:08:01
 Job time : 8.85924 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 ; Search time 27.0707 Seconds
(without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624
Sequence: 1 EVLVSGGDFVKGGLKV.....KLGTYRDSMGQTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/PCRS_PUBCOMB.pep:*
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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	624	100.0	130	9	US-09-764-304-18
2	624	100.0	130	14	US-10-265-713-18
3	624	100.0	130	14	US-10-166-626-18
4	614	98.4	130	9	US-09-764-304-8
5	614	98.4	130	14	US-10-265-713-8
6	614	98.4	130	14	US-10-166-626-8
7	487	78.0	134	17	US-10-477-377-8
8	486	77.9	140	13	US-10-006-773-4
9	481	77.1	121	14	US-10-276-939-3
10	475	76.1	119	14	US-10-281-479A-61
11	475	76.1	119	14	US-10-275-180A-61
12	475	76.1	119	14	US-10-286-132A-61
13	475	76.1	462	14	US-10-281-479A-23

14	475	76.1	462	14	US-10-286-132A-23	Sequence 23, Appl
15	475	76.1	464	14	US-10-275-180A-23	Sequence 23, Appl
16	473.5	75.9	120	15	US-10-412-406-2	Sequence 2, Appl
17	473.5	75.9	4852	15	US-10-412-406-33	Sequence 33, Appl
18	473	75.8	123	9	US-09-144-886-61	Sequence 61, Appl
19	473	75.8	123	16	US-10-632-706-58	Sequence 58, Appl
20	471	75.5	119	14	US-10-270-071-5	Sequence 5, Appl
21	471	75.5	119	14	US-10-270-071-6	Sequence 6, Appl
22	471	75.5	262	14	US-10-270-071-20	Sequence 20, Appl
23	471	75.5	262	14	US-10-270-071-24	Sequence 24, Appl
24	471	75.5	262	14	US-10-270-071-28	Sequence 28, Appl
25	471	75.5	268	14	US-10-270-071-10	Sequence 10, Appl
26	471	75.5	268	14	US-10-270-071-12	Sequence 12, Appl
27	471	75.5	268	14	US-10-270-071-16	Sequence 16, Appl
28	471	75.5	268	14	US-10-328-190-12	Sequence 12, Appl
29	471	75.5	415	14	US-10-328-190-12	Sequence 12, Appl
30	469	75.2	262	14	US-10-270-071-34	Sequence 34, Appl
31	469	75.2	268	14	US-10-270-071-32	Sequence 32, Appl
32	469	75.2	268	14	US-10-328-190-2	Sequence 2, Appl
33	469	75.2	268	14	US-10-328-190-4	Sequence 4, Appl
34	468.5	75.1	118	9	US-09-423-800-46	Sequence 46, Appl
35	468.5	75.1	118	14	US-10-182-018-46	Sequence 46, Appl
36	468.5	75.1	118	14	US-10-169-003-46	Sequence 46, Appl
37	468.5	75.1	118	14	US-10-337-981-46	Sequence 46, Appl
38	468.5	75.1	118	15	US-10-344-733-46	Sequence 46, Appl
39	468.5	75.1	137	9	US-09-423-800-76	Sequence 76, Appl
40	468.5	75.1	137	14	US-10-337-981-76	Sequence 76, Appl
41	468	75.0	125	11	US-09-910-358D-4	Sequence 4, Appl
42	468	75.0	125	11	US-09-910-358D-8	Sequence 8, Appl
43	468	75.0	140	9	US-09-286-140-4	Sequence 4, Appl
44	468	75.0	144	9	US-09-881-823-12	Sequence 12, Appl
45	468	75.0	155	14	US-10-077-624-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-764-304-18
; Sequence 18, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KIWANA, YOSHITISHA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; EARLIER FILING DATE: 2001-01-19
; EARLIER APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; EARLIER APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; EARLIER APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; EARLIER APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CDNA KM-641
US-09-764-304-18

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Query Match          100.0%; Score 624; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 2,6e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 60
      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
DB      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
QY      61 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 119
      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129
DB      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129

RESULT 2
US-10-265-713-18
; Sequence 18, Application US/10265713
; Publication No. US2003009564A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/265,713
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/225,322
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-265-713-18

Query Match          100.0%; Score 624; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 2,6e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
DB      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
QY      61 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 119
      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129
DB      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129

RESULT 3
US-10-166-626-18
; Sequence 18, Application US/10166626
; Publication No. US20030166876A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
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; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/10/166,626
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; PRIOR FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-18

Query Match          100.0%; Score 624; DB 14; Length 130;
Best Local Similarity 100.0%; Pred. No. 2,6e-50;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 60
      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
DB      11 EVTLVSGGDFVKPGGSLKVSQAASGFAPSHYAMSVWROTPAKRLEWVAIYISGGSGITY 70
QY      61 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 119
      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129
DB      71 SDSVGRFTISRDNANKNTLYLQMRSLRSDSAMVFCIRVKLGITYYFDSWGQGTTLTVSS 129

RESULT 4
US-09-764-304-8
; Sequence 8, Application US/09764304
; Patent No. US2002026036A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KUMANA, YOSHIHISA
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/764,304
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 09/225,322
; EARLIER FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; EARLIER FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; EARLIER FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; EARLIER FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; EARLIER FILING DATE: 1992-09-17
; EARLIER APPLICATION NUMBER: JP 3-238375
; EARLIER FILING DATE: 1991-09-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: cDNA KM-641
US-09-764-304-8
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 Db 121 S 121

RESULT 8
US-10-006-773-4

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: Sequence 4, Application US/10006773
: Publication No. US20020132983A1
: GENERAL INFORMATION:
: APPLICANT: Jungmans, Richard P.
: TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti-
: FILE REFERENCE: 003
: CURRENT APPLICATION NUMBER: US/10/006,773
: CURRENT FILING DATE: 2001-12-10
: PRIOR APPLICATION NUMBER: 60/250,089
: PRIOR FILING DATE: 2000-11-30
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 140
: TYPE: PRT
: ORGANISM: Mus sp.
: US-10-006-773-4

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Query Match	77.9%;	Score 486;	DB 13;	Length 140;
Best Local Similarity	77.7%;	Pred. No. 1.9e-37;		
Matches 94;	Conservative 9;	Mismatches 16;	Indels 2;	Gaps 1

[illegible]

RESULT 9
US-10-276-939-3

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? Sequence 3 Application US/10276939
? Publication No. US20030215450A1
? GENERAL INFORMATION:
? APPLICANT: BLAKE, SIMON M.
? APPLICANT: SWEET, RAYMOND W.
? APPLICANT: TAYLOR, ALEXANDER H.
? APPLICANT: WATTAM, TREVOR A.
? TITLE OF INVENTION: Anti-RANK Ligand Monoclonal Antibodies
? TITLE OF INVENTION: Useful in Treatment of RANK Ligand Mediated Disorders
? FILE REFERENCE: GP50024
? CURRENT APPLICATION NUMBER: US/10/276,939
? CURRENT FILING DATE: 2002-11-21
? PRIOR APPLICATION NUMBER: PCT/US01/16865
? PRIOR FILING DATE: 2001-05-24
? PRIOR APPLICATION NUMBER: 60/207,628
? PRIOR FILING DATE: 2000-05-26
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 3
? LENGTH: 121
? TYPE: PRT
? ORGANISM: Murine
? US-10-276-939-3

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Query Match	77.1%;	Score 481;	DB 14;	Length 121;
Best Local Similarity	78.5%;	Pred. No. 4.7e-37;		

Matches 95; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

QY 1 EYLVASSGGDFFYKPGGSLVSCAASGAFPSHAAAMWVWQTPKXRLIEWAWYISGGSSGTY 60
QY 2 EYLVASSGGDFFYKPGGSLVSCAASGAFPSHAAAMWVWQTPKXRLIEWAWYISGGSSGTY 60
Db 1 EVLVASSGGDLVYKPGGSLVSCAASGFTFSRGGMAWVWQTPKXRLIEWAWYISGGSYTY 60
QY 61 SDSVKKRFTTISRDNANNTLYLQMRSLRSDSAMFYCTRVKLGTY--YDSSNGQGTLTVS 111
QY 61 PDSVKKRFTTISRDNANNTLYLQMRSLRSDSAMFYCTRVKLGTY--YDSSNGQGTLTVS 111
Db 61 PDSVKKRFTTISRDNANNTLYLQMRSLRSDSAMFYCTRVKLGTY--YDSSNGQGTLTVS 120

Qy	119 S	119
Db	121 S	121

RESULT 10
US-10-281

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Sequence 61. Application US/10281479A
Publication No. US20030133932A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oehmli, Jun
APPLICANT: Lobuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-61

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Query Match	76.1%	Score 475;	DB 14;	Length 119;
Best Local Similarity	79.8%	Pred. No. 1.7e-36;		
Matches 95; Conservative	3;	Mismatches 21;	Indels 0;	Gaps 0;

[illegible]

RESULT 11
US-10-275

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; Sequence 61, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa

```

APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
FILE REFERENCE: 21085.002905
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: /No. US20030190687A1e =
US-10-275-180A-61

Query Match 76.1%; Score 475; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,7e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

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DB 1 EYLVESGGGLVYKPGSLKXSCASGFTFSYVMSWRQTPKRLKLEWVAIYSSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 119
DB 61 PDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 119

RESULT 12

US-10-286-132A-61
Sequence 61, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Lobjuglio, Albert S.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002907
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: /No. US20030198637A1e = Synth

US-10-286-132A-61

Query Match 76.1%; Score 475; DB 14; Length 119;
Best Local Similarity 79.8%; Pred. No. 1,7e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYLVESGDFVYKPGSLKXSCASGAFBSHYAMSWRQTPAKKLEWVAIYSSGSGSTYY 60
DB 1 EYLVESGGGLVYKPGSLKXSCASGFTFSYVMSWRQTPKRLKLEWVAIYSSGSGSTYY 60
QY 61 SDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 119
DB 61 PDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 119

RESULT 13
US-10-281-479A-23
Sequence 23, Application US/10281479A
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
APPLICANT: Lobjuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THE
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: /No. US2003013932A1e = Synth

US-10-281-479A-23

Query Match 76.1%; Score 475; DB 14; Length 462;
Best Local Similarity 79.8%; Pred. No. 6,8e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 1 EYLVESGDFVYKPGSLKXSCASGAFBSHYAMSWRQTPAKKLEWVAIYSSGSGSTYY 60
DB 20 EYLVESGGGLVYKPGSLKXSCASGFTFSYVMSWRQTPKRLKLEWVAIYSSGSGSTYY 79
QY 61 SDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 119
DB 80 PDSVKGRFTISRDNKATLYLQMSLSRSEDSAMFCTRYVKGTYYPDSMGQGTTLTVSS 138

RESULT 14

US-10-286-132A-23
Sequence 23, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Lobjuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.002907
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02

US-10-286-132A-23

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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-23
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Query Match          76.1%; Score 475; DB 14; Length 462;
Best Local Similarity 79.8%; Pred. No. 6.8e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
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Db      20 EYLVESGGGLVYKPGGSLKVCASGFTSSYVMSWVROTPEKRLKEMVAIYISGSGSTYY 79
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY      61 SDSVKGRFTISRDNANTLYLQMSLRSESDSAMYFCTRYVLTGYFPDSWGQGTTLTVSS 119
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      80 PDSVKGRFTISRDNANTLYLQMSLRSEDTAMYCARGDSDMITTDYWGQGTTLTVSS 138
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RESULT 15

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US-10-275-180A-23
; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimhisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275,180A
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
US-10-275-180A-23
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Query Match          76.1%; Score 475; DB 14; Length 464;
Best Local Similarity 79.8%; Pred. No. 6.8e-36;
Matches 95; Conservative 3; Mismatches 21; Indels 0; Gaps 0;
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QY      1 EYLVESGGDFVYKPGGSLKVCASGAFSHYAMSWVROTPAKRLKEMVAIYISGSGSTYY 60
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      20 EYLVESGGGLVYKPGGSLKVCASGFTSSYVMSWVROTPEKRLKEMVAIYISGSGSTYY 79
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY      61 SDSVKGRFTISRDNANTLYLQMSLRSESDSAMYFCTRYVLTGYFPDSWGQGTTLTVSS 119
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      80 PDSVKGRFTISRDNANTLYLQMSLRSEDTAMYCARGDSDMITTDYWGQGTTLTVSS 138
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Search completed: December 23, 2004, 19:35:48
Job time : 28.0707 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 6.43029 Seconds
(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-55

Perfect score: 624
Sequence: 1 EVTLVESGDPFVKGSLKV.....KLGRYFDSMGQTTLTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479	76.8	119	2 B34353	anti-peptide Fab'
2	471	75.5	120	2 S55536	Ig heavy chain V r
3	470.5	75.4	121	2 I27887	Ig heavy chain V r
4	469	75.2	120	2 S55537	Ig heavy chain V r
5	469	75.2	122	2 E27888	Ig heavy chain V r
6	467	74.8	111	2 PH1007	Ig heavy chain V r
7	466.5	74.8	119	2 F27888	Ig heavy chain V r
8	464	74.4	138	2 S09258	Ig heavy chain V r
9	463	74.2	120	2 S55539	Ig heavy chain V r
10	462.5	74.1	118	2 PH0097	Ig heavy chain V r
11	461	73.9	117	2 S20641	Ig heavy chain V r
12	461	73.9	117	2 PL0249	Ig heavy chain V r
13	460	73.7	120	2 S55538	Ig heavy chain V r
14	457.5	73.3	254	2 PH0096	Ig heavy chain V r
15	456.5	73.2	118	2 PH0096	Ig heavy chain V r
16	456	73.1	119	2 S31107	Ig heavy chain V r
17	456	73.1	124	2 C27888	Ig heavy chain V r
18	456	73.1	138	2 S31666	Ig heavy chain V r
19	455.5	73.0	112	2 S26347	Ig heavy chain V r
20	454	72.8	117	2 PL0252	Ig heavy chain V r
21	452.5	72.5	121	2 A27888	Ig heavy chain V r
22	452.5	72.5	121	2 S55540	Ig heavy chain V r
23	451.5	72.4	121	2 D27888	Ig heavy chain V r
24	451.5	72.4	121	2 B27888	Ig heavy chain V r
25	450.5	72.2	119	2 D27889	Ig heavy chain V r
26	449.5	72.0	113	2 S26468	Ig heavy chain V r
27	449.5	72.0	121	2 H27887	Ig heavy chain V r
28	448.5	71.9	139	2 S38808	Ig heavy chain - m
29	447.5	71.7	548	2 S38864	Ig epsilon chain C

30	447	71.6	152	2 B26471	Ig heavy chain pre
31	446.5	71.6	138	2 S26790	Ig heavy chain V r
32	444.5	71.2	119	2 B27889	Ig heavy chain V r
33	443.5	71.1	121	2 H27888	Ig heavy chain V r
34	443	71.0	119	2 PH0098	Ig heavy chain V r
35	442	70.8	124	2 I27888	Ig heavy chain V r
36	441.5	70.8	108	2 PH1010	Ig heavy chain V r
37	441.5	70.8	118	2 S31105	Ig heavy chain (eu
38	441	70.7	119	2 D36005	Ig heavy chain V r
39	440	70.5	125	2 S30531	Ig heavy chain V r
40	439.5	70.4	120	2 S12953	Ig heavy chain V r
41	439.5	70.4	123	2 S63597	Ig heavy chain V r
42	439	70.4	119	2 S31108	Ig heavy chain - h
43	438.5	70.3	123	2 G27888	Ig heavy chain V r
44	438	70.2	140	2 S31686	Ig heavy chain V r
45	437.5	70.1	140	2 S70442	Ig heavy chain pre

ALIGNMENTS

RESULT 1

anti-peptide Fab' B132 heavy chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 23-Jul-1999

C/Accession: B34353

R/Stura, E.A.; Stanfield, R.L.; Fieser, T.M.; Balderas, R.S.; Smith, L.R.; Lerner, R.A.

J. Biol. Chem. 264, 15721-15725, 1989

A/Title: Preliminary crystallographic data and primary sequence for anti-peptide Fab' B

A/Reference number: A34353; MUID:89359424; PMID:2504725

A/Accession: B34353

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-119 <STU>

A/Cross-references: GB:M29252; NID:g195657; PIDN:AAA388.1; PID:g195658

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:1598/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 479; DB 2; Length 119;

Best Local Similarity 78.2%; Pred. No. 1.3e-37;

Matches 93; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 1 EVTLVESGDPFVKGSLKVCASGAFSHYMSVROTPAKLEVAIVISGSGSTTY 60

DB 1 EVTLVESGDPFVKGSLKVCASGAFSHYMSVROTPAKLEVAIVISGSGSTTY 60

OY 61 SDSVKGFRFTSRDANKVTLQWRSLRSEDSNAYFCTRVKLGTYVPDSMGQTTLTIVSS 119

DB 61 PDIYKGRFTISRDNARNTLSLQMSLRSEDTALTYCTRVSSDPFYDYGQTTLTIVSS 119

RESULT 2

Ig heavy chain V region pe20 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C/Accession: S55536

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usi

utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55536

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <BOE>

A/Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 471; DB 2; Length 120;

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DE SCFV B8B5 protein (Fragment).
GN SCFV B8B5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=balb/c;
RA Peter J.C.; Mallukat G.; Tugler J.; Maurice D.; Roegel J.C.,
RA Briand J.P.; Hoebeke J.;
RT "Modulation of the M2 muscarinic receptor activity with monoclonal
RT anti-M2 receptor antibody fragments."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RD EMBL; AJ746180; CAG34081.1; -.
SQ NON TER 1 1
SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 75.2%; Score 469; DB 2; Length 255;
Best Local Similarity 77.0%; Pred. No. 4.3e-41;
Matches 94; Conservative 7; Mismatches 17; Indels 4; Gaps 2;

QY 1 EYTVESGGDFYKPGSLKVCASGPAFSHAMSVNRQTPAKRLFWAVYISSGSGTTY 60
DB 1 QYVLOQSGGDLVYKPGSLKVCASGFTFSSYGMVNRQTPDKRLFWAVYISSGSGTTY 60

QY 61 SDSVGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTY--FDPMGCGTTLV 117
DB 61 PDSVGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTY--FDPMGCGTTLV 117

QY 118 SS 119
DB 120 SS 121

RESULT 3
Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LOC380791 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
RA Altshul S.F.; Zeeberg B.; Buettow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Heish F.;
RA Diatchenko L.; Musina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Ustin L.B.; Toshlyuk S.; Carninci P.; Frange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gurnatne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Pahay J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko J.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;
RA Krzywicki M.I.; Skalska U.; Smalins D.E.; Scherch A.; Schein J.E.;
RA Jones S.J.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RA Strausberg R.L.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RD EMBL; BC004786; AAH04786.1; -.
DR HSSP; P01810; 2Fab.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
SQ NON TER 1 1
SEQUENCE 487 AA; 52554 MW; 7DC8E96DB33077B CRC64;

Query Match 75.1%; Score 468.5; DB 2; Length 487;
Best Local Similarity 75.0%; Pred. No. 1e-40;
Matches 93; Conservative 7; Mismatches 19; Indels 5; Gaps 1;

QY 1 EYTVESGGDFYKPGSLKVCASGPAFSHAMSVNRQTPAKRLFWAVYISSGSGTTY 60
DB 20 EYVLOVESGGGLVYKPGSLKVCASGFTFSSYAMSVNRQTPDKRLFWAVYISSGSGTTY 79

QY 61 SDSVGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTY--FDPMGCGTTLV 115
DB 80 PDSVGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTY--FDPMGCGTTLV 139

QY 116 TVSS 119
DB 140 TVSS 143

RESULT 4
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Atkin J.D.; Jape A.; Jennings I.G.; Horatis O.; Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RD EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
SQ NON TER 1 1
SEQUENCE 119 AA; 13025 MW; F6E90404381CA7C CRC64;

Query Match 74.2%; Score 463; DB 2; Length 119;
Best Local Similarity 77.7%; Pred. No. 7.8e-41;
Matches 94; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

QY 1 EYTVESGGDFYKPGSLKVCASGPAFSHAMSVNRQTPAKRLFWAVYISSGSGTTY 60
DB 1 EYVLOVESGGDLVYKPGSLKVCASGFTFSSYGMVNRQTPDKRLFWAVYISSGSGTTY 60

QY 61 SDSVGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRYKLGTY--YFDSMGCGTTLTVS 118

Db 61 PDVSKGFRTISRDNKNTLYLQWRSLSRSDSAMYFCTRYLGTGTY-----YFDSWGGSTTL 118
QY 119 S 119
Db 119 A 119
RESULT 5
ID Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE LOC380791 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedln T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.
RA Strauberg R.L.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;
Query Match 72.9%; Score 455; DB 2; Length 486;
Best Local Similarity 71.0%; Pred. No. 2.7e-39;
Matches 86; Conservative 16; Mismatches 16; Indels 6; Gaps 2;
QY 1 EVTLVBSGGDFVFKGSLKVCSCAASGPAFHSYAMSVRQTPAKLEWVAIYSSGSGSTTY 60
Db 20 EVTLVBSGGGLVFKGSLKVCSCAASGPAFHSYAMSVRQTPAKLEWVAIYSSGSGSTTY 78

QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYLGTGTY-----YFDSWGGSTTL 115
Db 79 PDVSKGFRTISRDNKNTLYLQWRSLSRSDSAMYFCTRYLGTGTY-----YFDSWGGSTTL 138
QY 116 TVSS 119
Db 139 TVSS 142
RESULT 6
ID Q91WPS PRELIMINARY; PRT; 479 AA.
AC Q91WPS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedln T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywnicki M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strauberg R.L.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013656; AAH13656.1; -
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;
Query Match 72.1%; Score 450; DB 2; Length 479;
Best Local Similarity 73.9%; Pred. No. 8.9e-39;
Matches 88; Conservative 9; Mismatches 18; Indels 4; Gaps 1;
QY 1 EVTLVBSGGDFVFKGSLKVCSCAASGPAFHSYAMSVRQTPAKLEWVAIYSSGSGSTTY 60
Db 20 EVTLVBSGGGLVFKGSLKVCSCAASGPAFHSYAMSVRQTPAKLEWVAIYSSGSGSTTY 79
QY 61 SDSVKGRFTISRDNKNTLYLQWRSLSRSDSAMYFCTRYLGTGTY-----YFDSWGGSTTL 115

[illegible][illegible]

Query Match 69.7%; Score 435; DB 2; Length 124;
Best Local Similarity 66.9%; Pred. No. 7.3e-38;
Matches 81; Conservative 17; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVTLVESGDPVKPGSLKVCASGAFSHYAMSWRQTPAKKLEWVAIISGGSGTTY 60
1 QVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMWVRQAPKGLEWVSTIKSAAGSTYY 60
DB 61 SDSVKGRFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 118
1 ADGVKGRFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 120
QY 119 S 119
121 S 121
DB

RESULT 10
BAD00491 PRELIMINARY; PRT; 125 AA.
ID BAD00491; PRT; 125 AA.
AC BAD00491; PRT; 125 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain VHJ region (Fragment).
GN IGVH
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Honda T., Akahori Y., Kurosawa Y.;
RT "Libraries of heavy-chain antibodies reflecting camel gamma2 and
RT gamma3 in vivo repertoires."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB092129; BAD00491.1; -.
FT NON_TER 1
FT NON_TER 125
SQ SEQUENCE 125 AA; 13593 MW; F1637892B028E48C CRC64;

Query Match 69.5%; Score 433.5; DB 2; Length 125;
Best Local Similarity 67.2%; Pred. No. 1.1e-37;
Matches 82; Conservative 18; Mismatches 19; Indels 3; Gaps 1;

QY 1 EVTLVESGDPVKPGSLKVCASGAFSHYAMSWRQTPAKKLEWVAIISGGSGTTY 60
1 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMWVRQAPKGLEWVAIISGGSTYY 60
DB 61 SDSVKGRFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 117
1 TESVKGKFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 120
QY 118 S 119
121 S 122
DB

RESULT 11
AAL35877 PRELIMINARY; PRT; 117 AA.
ID AAL35877; PRT; 117 AA.
AC AAL35877; PRT; 117 AA.
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Immunoglobulin heavy chain variable domain (Fragment).
OS Lama glama (Llama).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22007448; PubMed=12009207;
RA Tanha J., Dubuc G., Hiyama T., Nierang S.A., Mackenzie C.R.;
RT "Selection by phage display of llama conventional VH fragments with
RT heavy chain antibody VH(H) properties."
RL J. Immunol. Methods 263:97-109(2002).
DR EMBL: AF442946; AAL35877.1; -.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 12459 MW; 08F5E4BA402F98D1 CRC64;

Query Match 69.4%; Score 433; DB 2; Length 117;
Best Local Similarity 68.9%; Pred. No. 1.1e-37;
Matches 82; Conservative 15; Mismatches 20; Indels 2; Gaps 1;

QY 1 EVTLVESGDPVKPGSLKVCASGAFSHYAMSWRQTPAKKLEWVAIISGGSGTTY 60
1 EVQLVDSGGGLVQPGGSLRLSCAASGFTFSYAMWVRQAPKGLEWVSTIKSAAGSTYY 60
DB 61 SDSVKGRFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 119
1 ADGVKGRFTISRDAKNTLVYQMRSLSSEDSAMFCTRVKLTGYTPDS--WGQTTLTYS 117

RESULT 12
O6GMV2 PRELIMINARY; PRT; 606 AA.
ID O6GMV2; PRT; 606 AA.
AC O6GMV2; PRT; 606 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Maier M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073758; AAL35877.1; -.
DR InterPro: IPR003599; Ig
DR InterPro: IPR007110; Ig-like
DR InterPro: IPR003597; Ig_C1
DR InterPro: IPR003596; Ig_V
DR Pfam: PF07654; C1-ec; 4.
DR Pfam: PF00047; Ig; 4.

DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 69.2%; Score 431.5; DB 2; Length 606;
Best Local Similarity 64.2%; Pred. No. 1e-36;
Matches 86; Conservative 13; Mismatches 20; Indels 15; Gaps 2;

QY 1 EYTLVSGGDFYKPGGSLKVCASGPAFSPHYAMVWROTPAKRLLEWAVYISGSGGTTY 60
DB 20 QVQLVSGGGLVPRGGSILRLSCAASGFTPSDYMSWIRQAPGKLEWVSYISSSSYTMY 79
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR-----YKLTYYF--- 106
DB 80 ADSVKGRFTISRDNKNSLYLQMSLRABDTAVYCAARGNGIAAGRVVYADYXXYYG 139
QY 107 -DSWGQGTTLTVSS 119
DB 140 MDVWGQGTIVTVSS 153

RESULT 13

HV55 MOUSE

ID HV55 MOUSE STANDARD; PRT; 117 AA.

AC P18526;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig heavy chain V region 345 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10990;

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/cJ;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during the

RT primary immune response."

RL J. Exp. Med. 169:2007-2019(1989).

CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR: J05002; HYMS34.

DR HSSP: P01783; IIGC.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1

FT CHAIN 20 117 Ig heavy chain V region 345.

FT DOMAIN 20 49 Framework-1.

FT DOMAIN 50 54 Complementarity-determining-1.

FT DOMAIN 55 68 Framework-2.

FT DOMAIN 69 85 Complementarity-determining-2.

FT DOMAIN 86 117 Framework-3.

FT DISULFID 41 115 By similarity.

FT NON_TER 117

SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 69.1%; Score 431; DB 1; Length 117;
Best Local Similarity 83.7%; Pred. No. 1.8e-37;
Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 EYTLVSGGDFYKPGGSLKVCASGPAFSPHYAMVWROTPAKRLLEWAVYISGSGGTTY 60
DB 20 EYQLVSGGGLVPRGGSILRLSCAASGFTPSDYMSWIRQAPGKLEWVSYISSSSYTMY 79

QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTR 98
DB 80 PDTVGRFTISRDNKNTLYLQMSLRABDTAVYCAARGNGIAAGRVVYADYXXYYG 117

RESULT 14

Q9UL71

ID Q9UL71 PRELIMINARY; PRT; 121 AA.

AC Q9UL71;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035043; AAD56279.1; -.

DR HSSP: P01852; INPD.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 68.9%; Score 430; DB 2; Length 121;
Best Local Similarity 67.8%; Pred. No. 2.4e-37;
Matches 82; Conservative 14; Mismatches 23; Indels 2; Gaps 1;

QY 1 EYTLVSGGDFYKPGGSLKVCASGPAFSPHYAMVWROTPAKRLLEWAVYISGSGGTTY 60
DB 1 EYQLVSGGGLVPRGGSILRLSCAASGFTPSDYMSWIRQAPGKLEWVSYISSSSYTMY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRSLRSEDSAMYFCTRVLGTY--FDSWGQGTTLTVS 118
DB 61 ADSVKGRFTISRDNKNSLYLQMSLRABDTAVYCAARGNGIAAGRVVYADYXXYYG 120

QY 119 S 119
DB 121 S 121

RESULT 15

Q91XE1

ID Q91XE1 PRELIMINARY; PRT; 480 AA.

AC Q91XE1;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Igh-VJ558 protein (Fragment).

GN Name=Igh-VJ558;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feilgold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 28.8913 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DIQMTQTASSLPASLGDNRVT.....HQSKEPWTGCGTKLEIKR 108

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2000s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	108	AAB81990	Aab81990 Ganglioside
2	572	100.0	108	ABU11013	ABU11013 Modified
3	572	100.0	128	AAB01628	Aab01628 Murine Im
4	572	100.0	128	AAB81978	Aab81978 Ganglioside
5	572	100.0	128	ABU11003	ABU11003 Modified
6	564	98.6	128	AAV28368	AAV28368 pKM641 LA
7	562	97.4	128	AAR33257	Aar33257 Rat Immun
8	557	97.4	128	AAR53340	Aar53340 KM641 H C
9	521	91.1	108	AAW00834	AAW00834 Variable
10	520	90.9	127	AAAR12359	AAAR12359 Light (Ka
11	516	90.2	108	AAW04177	AAW04177 Variant V
12	516	90.2	108	AAW16620	AAW16620 Anti-huma
13	516	90.2	128	AAB81998	Aab81998 Ganglioside
14	516	90.2	650	ABR62591	ABR62591 Anti-CD7
15	516	90.2	651	ABR62590	ABR62590 Anti-CD7
16	515	90.0	126	AAAR12237	AAAR12237 Mouse Mab
17	514	89.9	108	AAB81988	Aab81988 Ganglioside
18	514	89.9	128	AAB81999	Aab81999 Ganglioside
19	511	89.3	128	AAB81992	Aab81992 Ganglioside
20	510	89.2	108	AAW70620	AAW70620 Anti-VEGF
21	510	89.2	108	ABP61189	ABP61189 Murine an
22	508	88.8	108	ABU11011	ABU11011 Modified
23	507	88.6	128	AAB81994	Aab81994 Ganglioside
24	507	88.6	214	ADN41870	Adn41870 Amino aci
25	506	88.5	128	AAB81995	Aab81995 Ganglioside

ALIGNMENTS

RESULT 1	AB81990	standard; protein; 108 AA.
XX	ID	AAB81990;
XX	AC	AAB81990;
XX	DT	03-JUL-2001 (first entry)
XX	DE	Ganglioside GD3 specific antibody related protein SEQ ID NO: 56.
XX	KW	Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX	KW	cancer.
XX	OS	Mus musculus.
XX	PN	W0200123432-A1.
XX	PD	05-APR-2001.
XX	PF	29-SEP-2000; 2000WO-JP006774.
XX	PR	30-SEP-1999; 99JP-00278291.
XX	PR	06-APR-2000; 2000JP-00105088.
XX	PA	(KYOW) KYOWA HAKKO KOGYO KK.
XX	PI	Hanai N, Shitara K, Nakamura K, Niwa R;
XX	DR	WPI; 2001-266143/27.
XX	PT	New human type complementation-determining region-transplanted antibody
XX	PT	and derivatives against ganglioside GD3, useful in diagnosis and therapy
XX	PT	of e.g. tumors, with low antigenicity, little side effects but potent
XX	PT	activity in cancer.
XX	PS	Claim 11; Page 174-175; 183pp; Japanese.
XX	CC	The present invention describes a monoclonal antibody which can react
XX	CC	specifically with ganglioside GD3. The antibody and its derivatives are
XX	CC	useful in the diagnosis and therapy of tumors, particularly cancer
XX	CC	diagnosis. The present sequence is a protein used in the exemplification
XX	CC	of the invention
XX	CC	Sequence 108 AA;
XX	CC	Sequence 108 AA;
XX	CC	Best Local Similarity 100.0%; Score 572; DB 4; Length 108;
XX	CC	Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM cancer.
 XX
 XX Mus musculus.
 OS
 PN WO200123432-A1.
 XX
 XX
 PD 05-APR-2001.
 XX
 XX 29-SEP-2000; 2000WO-JP006774.
 PF
 XX 30-SEP-1999; 99JP-00278291.
 PR
 XX 06-APR-2000; 2000JP-00105088.
 XX
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Hanai N, Shitara K, Nakamura K, Niwa R;
 PI
 XX WPI; 2001-266143/27.
 DR
 XX
 PT New human type complementation-determining region-transplanted antibody
 PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
 PT of e.g. tumors, with low antigenicity, little side effects but potent
 PT activity in cancer.
 PS
 XX Example 1; Page 140; 183pp; Japanese.
 CC The present invention describes a monoclonal antibody which can react
 CC specifically with ganglioside GD3. The antibody and its derivatives are
 CC useful in the diagnosis and therapy of tumors, particularly cancer
 CC diagnosis. The present sequence is a protein used in the exemplification
 CC of the invention
 CC
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 572; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.9e-39;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVPS 60
 DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVPS 80
 QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGCTKLEIKR 108
 DB 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGCTKLEIKR 128
 RESULT 5
 ABU11003
 ID ABU11003 standard; protein; 128 AA.
 XX
 AC ABU11003;
 XX
 DT 04-FEB-2003 (first entry)
 XX
 DE Modified ganglioside GD3 antibody associated protein #2.
 XX
 KM Ganglioside GD3; anti-ganglioside GD3 antibody; tumour; melanoma.
 XX
 OS Mus musculus.
 XX
 PN WO200278739-A1.
 XX
 PD 10-OCT-2002.
 XX
 XX 29-MAR-2002; 2002WO-JP003170.
 PF
 XX 29-MAR-2001; 2001JP-00097483.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Shitara K, Niwa R, Kanazawa J, Asada M;
 PI
 XX

DR WPI; 2003-067410/06.
 XX
 XX
 PT Drugs containing genetically-modified antibody against ganglioside GD3,
 PT its fragment, immunocompetent cell activators or/and antitumor agents in
 PT combination, applicable in treating malignant tumor like melanoma.
 PS
 XX Example 3; Page 98; 121pp; Japanese.
 CC The invention describes drugs contain a genetically-modified antibody
 CC against ganglioside GD3 or its fragment and at least 1 of a substance
 CC capable of activating immunocompetent cells and a substance having an
 CC antitumor activity in combination. The drugs can be used to treat tumour
 CC like melanoma and can provide a treatment with enhanced therapeutic
 CC effect and little side-reactions, particularly to relieve problems of
 CC side-effects during the conventional single administration. This sequence
 CC represents a protein associated with the anti- ganglioside GD3 antibody
 CC
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 572; DB 6; Length 128;
 Best Local Similarity 100.0%; Pred. No. 3.9e-39;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVPS 60
 DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVPS 80
 QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGCTKLEIKR 108
 DB 81 RFSGGSGTDYSLTISNLEPEDIATYFCHQYSKLPMTFGGCTKLEIKR 128
 RESULT 6
 AAY28368
 ID AAY28368 standard; protein; 128 AA.
 XX
 AC AAY28368;
 XX
 DT 04-NOV-1999 (first entry)
 XX
 DE pKM641 LA2 immunoglobulin light chain.
 XX
 KM antibody; nucleotide; genomic; hypervariable region; chimeric;
 KM light chain; amino acid.
 XX
 OS Mus sp.
 XX
 PN US5939532-A.
 XX
 PD 17-AUG-1999.
 XX
 PF 07-JUN-1995; 95US-00483528.
 XX
 PR 07-SEP-1993; 93US-00116778.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakamura K, Hanai N, Kuwana Y, Hasegawa M, Koike M, Shitara K;
 XX
 DR WPI; 1999-468416/39.
 XX
 DR N-PSDB; AAX99481.
 XX
 PT Chimeric human antibody expression vectors.
 PS
 XX Example 1; Col 99; 188pp; English.
 CC This immunoglobulin region was isolated from pKM641LA2, A methionine
 CC codon, presumably the initiation codon ATG, was found in the vicinity of
 CC the 5' terminus and the sequence has a full length leader sequence. The
 CC chimeric human antibodies are useful in the treatment of cancer,
 CC especially that which is of neural ectodermal origin. In contrast to
 CC prior art constructs based on mouse monoclonal antibodies, the chimeric
 CC human antibodies do not cause anti-mouse immunoglobulin production. The

CC chimeric human antibodies have a prolonged half-life and a reduced
 CC frequency of adverse effects when compared to mouse monoclonal antibodies
 XX
 XX
 SO Sequence 128 AA;

Query Match 98.6%; Score 564; DB 2; Length 128;
 Best Local Similarity 99.1%; Pred. No. 1,7e-38;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 60
 DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 80

QY 61 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 108
 DB 81 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 128

RESULT 7

AAR33257
 ID AAR33257 standard; protein; 128 AA.

XX AAR33257;

DT 25-MAR-2003 (revised)
 DT 12-JUL-1993 (first entry)

DE Rat immunoglobulin L chain variable region of pKM6411A2.

KM Promoter; variable; region; rat; immunoglobulin; heavy; H; chain;
 KM humanised; chimeric; antibody; expression vector.

XX Rattus rattus.

Key Location/Qualifiers
 Peptide 1..20
 FT /note= "Signal peptide"
 FT 21..128
 FT /note= "Mature protein"

PN EP533199-A2.

XX 24-MAR-1993.

PF 18-SEP-1992; 92EP-00116026.

PR 18-SEP-1991; 91JP-00238375.

XX (KYOW) KYOWA HAKKO KOGYO CO LTD.

PI Shitara K, Hanai N, Hasegawa M, Miyaji H, Kuwana Y;

DR WPI; 1993-095510/12.

XX N-PSDB; AAQ33258.

PT Humanised chimeric antibody prodn. against ganglioside GD3 - for treating
 PT cancers, such as melanoma, neuroblastoma, etc.

PS Claim 6; Page 30-31; 63pp; English.

CC The sequences given in AAR33256-57 represent rat heavy and light chain
 CC variable regions respectively. The DNA sequences encoding these proteins
 CC were used in the construction of humanised chimeric antibody expression
 CC vectors. In these humanised antibodies none of the amino acids of the non
 CC human animal Ab variable region have been changed. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 128 AA;

Query Match 98.3%; Score 562; DB 2; Length 128;
 Best Local Similarity 99.1%; Pred. No. 2.5e-38;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 60
 DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 80

QY 61 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 108
 DB 81 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 128

RESULT 8

AAR53340
 ID AAR53340 standard; protein; 128 AA.

XX AAR53340;

DT 18-NOV-1994 (first entry)

DE KM641 H chain variable region.

XX Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody;
 XX expression vector; heavy; light; chain; hypervariable region; CDR;
 XX constant region; hybridoma; Ig; immunoglobulin; promoter; enhancer.

XX Mus musculus.

Key Location/Qualifiers
 Peptide 1..20
 FT /label= sig_peptide

PN AU9346181-A.

PD 17-MAR-1994.

PF 07-SEP-1993; 93AU-00046181.

PR 07-SEP-1992; 92JP-00238452.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakamura K, Koike M, Shitara K, Hanai N, Kuwana Y, Hasegawa M;

DR WPI; 1994-126857/16.

XX N-PSDB; AAQ5438.

PT Humanised antibody specific for ganglioside GM2 - used for producing a
 PT cytotoxic effect on cancers such as melanoma, neuroblastoma and glioma.

PS Example 2; Page 115-116; 191pp; English.

CC Example 2 describes the construction of the vector pCh1641HA1 for
 CC chimeric human antibody H chain expression. mRNA from mouse anti-GD3
 CC monoclonal Ab KM641-producing cells was isolated and KM641 H and L chain
 CC cDNAs isolated. The base sequences of the Ig variable regions in KM641 H
 CC chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2) are given in
 CC AAQ45438-39. A KM641-derived chimeric human Ab H chain expression vector
 CC was constructed by joining the H chain variable region gene from
 CC pKM641HA3 to a vector for chimeric human Ab H chain expression using the
 CC synthetic DNAs given in AAQ5439 and AAQ5440

XX Sequence 128 AA;

Query Match 97.4%; Score 557; DB 2; Length 128;
 Best Local Similarity 98.1%; Pred. No. 6.5e-38;
 Matches 106; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 60
 DB 21 DIQMTQTASSLPASLGDRVTISCSASQDISNLTMYQKPDGTVKLLIFYSNLSHGVP 80

QY 61 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 108
 DB 81 RFSGGSGGTDYSLTISNLEPEDIAITYFCHQYKLPWTFGGGTRKLEIKR 128

```

RESULT 9
AA000834
ID AAW00834 standard; protein; 108 AA.
XX
XX AAW00834;
XX
XX 20-MAY-1997 (first entry)
XX
XX Variable light chain of anti-human Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus.
XX
XX Mus musculus.
XX
XX WO9629350-A1.
XX
XX 26-SEP-1996.
XX
XX 21-MAR-1996; 96WO-JP000734.
XX
XX 20-MAR-1995; 95JP-00087420.
XX 27-OCT-1995; 95JP-00303492.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX Kayaagaki N, Yagita H, Okumura K, Nakata M;
XX WPI; 1996-443140/44.
XX N-PSDB; AAT39560.
XX
XX Monoclonal antibody specifically recognising the Fas ligand - useful for
XX the detection of Fas ligands either on cell surface or in solution.
XX
XX Claim 41; Page 93-94; 133pp; Japanese.
XX
XX The present sequence is the light chain variable region of the anti-human
XX Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by the
XX hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
XX with transformed human Fas ligand expressing COS cells, and fusing spleen
XX cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
XX cells. The Mab recognises the human Fas ligand on the cell surface or in
XX solution, and can be used to inhibit the apoptosis inducing cell surface
XX Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
XX in biological samples (e.g. human blood), especially for disease
XX diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
XX erythematosus
XX
XX Sequence 108 AA;
SQ
Query Match 91.1%; Score 521; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 4.7e-35;
Matches 99; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
OY 1 DIQWTTASSLPASLGRVTISCSASODISNYLWYQOKPDGTVKLLIFYSNNHSGVPS 60
DB 1 DIQWTTSSLSASLGRVTISCSASODISNYLWYQOKPDGTVKLLIFYSNNHSGVPS 60
OY 61 RFGSGSGTDYSLTISNLEPEDATYFCQYSLKLPWFGGATKLEIKR 108
DB 61 RFGSGSGTDYSLTISNLEPEDATYFCQYSLKLPWFGGATKLEIKR 108

RESULT 10
AA012359
ID AAR12359 standard; protein; 127 AA.
XX
XX AAR12359;
XX
XX 25-MAR-2003 (revised)
XX 15-AUG-1991 (first entry)

```

```

XX
XX Light (kappa) chain variable region of murine 1C11 immunoglobulin.
XX
XX Chimeric antibodies; immunconjugates; HIV; AIDS.
XX
XX Mus musculus.
XX
XX WO9107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1989; 89US-00433730.
XX
XX 13-NOV-1989; 89US-00433730.
XX
XX (XOMA ) XOMA CORP.
XX (GREC ) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghoshdastgi P, Robinson R;
XX WPI; 1991-178105/24.
XX N-PSDB; AAQ12061.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV
XX -1 antigen from sample.
XX
XX Disclosure; Fig 13; 107pp; English.
XX
XX This is the light (kappa) - chain variable (V) region of a mouse
XX monoclonal antibody (Mab), 1C11, and is specific for an HIV-1 viral
XX antigen. It is used in the construction of a chimeric Mab comprising
XX heavy and light chains having murine V regions and human C regions. The
XX chimeric Mabs are more effective than murine Mab 1C11 since they have an
XX increased compatibility in humans. The heavy and light chain V-regions
XX are joined by manipulating their respective joining (J) regions, to
XX generate restriction enzyme recognition sites. The chimeric Mabs can be
XX used as immunconjugates, in association with e.g. toxins for HIV
XX treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
XX 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
XX 60 and AAQ12062-63. (Updated on 25-MAR-2003 to correct PA field.)
XX correct DR field.)
XX
XX Sequence 127 AA;
SQ
Query Match 90.9%; Score 520; DB 2; Length 127;
Best Local Similarity 91.6%; Pred. No. 6.6e-35;
Matches 99; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 1 DIQWTTASSLPASLGRVTISCSASODISNYLWYQOKPDGTVKLLIFYSNNHSGVPS 60
DB 21 DIQWTTSSLSASLGRVTISCSASODISNYLWYQOKPDGTVKLLIFYSNNHSGVPS 80
OY 61 RFGSGSGTDYSLTISNLEPEDATYFCQYSLKLPWFGGATKLEIKR 107
DB 61 RFGSGSGTDYSLTISNLEPEDATYFCQYSLKLPWFGGATKLEIKR 127

RESULT 11
AA041777
ID AAW04177 standard; protein; 108 AA.
XX
XX AAW04177;
XX
XX 19-MAY-1997 (first entry)
XX
XX Variant variable light chain of Fas ligand antibody NOK-1.
XX
XX Variable region; light chain; human; Fas ligand; monoclonal; antibody;
XX NOK-1; hybridoma; inhibition; apoptosis; assay; diagnosis; disease;
XX hepatitis; infectious mononucleosis; systemic lupus erythematosus;
XX variant.
XX
XX Mus musculus.

```

XX MO9629350-A1.
PN
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-JF000734.
XX
PR 20-MAR-1995; 95JP-00087420.
PR 27-OCT-1995; 95JP-00303492.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
PI Kayagaki N, Yagita H, Okumura K, Nakata M;
XX
DR WPI; 1996-443140/44.
DR N-PSDB; AAT39550.
XX
PT Monoclonal antibody specifically recognising the Fas ligand - useful for
PT the detection of Fas ligands either on cell surface or in solution.
XX
PS Claim 20; Page 80-81; 133pp; Japanese.
XX
CC The present sequence is a variant light chain variable region of the anti
CC -human Fas ligand monoclonal antibody (Mab) NOK-1. NOK-1 is produced by
CC the hybridoma NOK-1 (FERM BP-5044), which was prepared by immunising mice
CC with transformed human Fas ligand expressing COS cells, and fusing spleen
CC cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580)
CC cells. The Mab recognises the human Fas ligand on the cell surface or in
CC solution, and can be used to inhibit the apoptosis inducing cell surface
CC Fas ligand/Fas reaction. The Mab can also be used for a Fas ligand assay
CC in biological samples (e.g. human blood), especially for disease
CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic lupus
CC erythematosus
XX
SQ Sequence 108 AA;
XX
Query Match 90.2%; Score 516; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASLPSLGDRTVITSCASQDISNYLNMWYQKPDGTVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASLGRTVITSCRASQDISNYLNMWYQKPDGTVKLIIFYTSLRHSGVPS 60
QY RFSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGTLEIKR 108
XX
RESULT 12
AAW16620
ID AAW16620 standard; protein; 108 AA.
XX
AC AAW16620;
XX
DT 14-JAN-1998 (first entry)
XX
DE Anti-human FasL antibody (NOK1) light chain variable region.
XX
KW light chain; variable region; mouse; murine; human; Fas ligand; FasL;
KW monoclonal antibody; Mab; hybridoma; treatment; hepatitis;
KW hepatitis B virus; HBV; hepatitis C virus; HCV; apoptosis; liver cell;
KW glutamate oxaloacetate; pyruvate transaminase.
XX
OS Mus sp.
XX
PN WO9715326-A1.
XX
PD 01-MAY-1997.
XX
PF 24-OCT-1996; 96WO-JP003089.
XX
PR 27-OCT-1995; 95JP-00303491.
XX

XX (SUME) SUMITOMO ELECTRIC IND CO.
PA
XX
PI Seino K, Kayagaki N, Yagita H, Okumura K, Nakata M;
XX
DR WPI; 1997-258767/23.
DR N-PSDB; AAT66710.
XX
PT Anti-human Fas ligand antibody to treat hepatitis - controls apoptosis in
PT liver cells and improves liver function.
XX
PS Claim 6; Page 30-31; 51pp; Japanese.
XX
CC The present sequence is the light chain variable region of the murine
CC anti-human Fas ligand (FasL) monoclonal antibody (Mab) NOK1, which is
CC expressed by the hybridoma NOK1 (FERM BP-5044). The Mab can be used in
CC the preparation of a composition for the effective oral or parenteral
CC treatment of hepatitis, including hepatitis caused by hepatitis B or C
CC virus. The composition controls apoptosis in liver cells caused by the
CC binding of FasL to Fas expressing liver cells, and improves liver
CC function by improving blood glutamate oxaloacetate and pyruvate
CC transaminase levels. The composition is given in a dosage of 0.0001-1000,
CC preferably 0.01-600 mg/day. Spleen cells from mice immunised with FasL
CC expressing COS cells were fused with mouse myeloma cells to produce
CC hybridomas. The hybridomas were screened for anti-FasL activity, and the
CC active clones NOK1-5 isolated
XX
SQ Sequence 108 AA;
XX
Query Match 90.2%; Score 516; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQTASLPSLGDRTVITSCASQDISNYLNMWYQKPDGTVKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQSPSSLSASLGRTVITSCRASQDISNYLNMWYQKPDGTVKLIIFYTSLRHSGVPS 60
QY RFSGGSGGTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTLEIKR 108
DB 61 RFSGSGSGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGTLEIKR 108
XX
RESULT 13
AAB81998
ID AAB81998 standard; protein; 128 AA.
XX
AC AAB81998;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein #7.
XX
KW Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105088.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
DR N-PSDB; AAF86912.
XX

Claim 9; Page 8; 55pp; English.

The present sequence is that of a novel fusion protein comprising an scFv fragment of anti-CD7 monoclonal antibody TH-69 and domains II and III of Pseudomonas exotoxin A (ETA), joined via a peptide linker, and including an N-terminal 6XHis tag and C-terminal KDEL sequence. This novel fusion protein binds to CD7-positive T-lymphoid cells and kills them by the induction of apoptosis. It is an example of anti-CD7 scFv immunotoxin fusion proteins of the invention. An expression vector, host cells, a method for producing the fusion protein, and a vaccine comprising the fusion protein are claimed. The fusion protein is used in the treatment of disorders involving a hyperproliferation of CD7-positive cells, especially acute T-cell and/or myeloid leukaemia, and also in the treatment or prophylaxis of graft-versus-host disease. A claimed method of conditioning an animal (e.g. a human) to be transplanted with donor cells, tissue or organ comprises: (a) depleting the CD7-bearing cell population in the animal; (b) providing a transplant comprising isolated bone marrow and/or stem cell-enriched peripheral blood cells of the donor, where the CD7-bearing cell population in (a) and/or the transplant in (b) are treated with a T-cell depleting effective amount of the fusion protein or therapeutic composition comprising the fusion protein; and (c) introducing the transplant into the animal

Sequence 650 AA;

Query Match 90.2%; Score 516; DB 6; Length 650;
Best Local Similarity 90.7%; Pred. No. 7,1e-34;
Matches 99; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

DY 1 DIQMTQTASSLPASLGDRVTISGASADISNYLNMWYOQKPDGYKLIIFFSYNSIHSGVPS 60
Db 17 DIQMTQTSSLSASIGDRTVITSCSASOGIANYLNMWYOQKDPDGYKLIIYTSSLHSGVPS 76
DY 61 RFGSGSGGTDTYSLTITSNLREPIDATYCHQYSKLPFRFGGTKEIKR 108
Db 77 RFGSGSGGTDTYSLTITSNLREPIDATYCCQYSKLPYTFGGGTKEIKR 124

RESULT 15
ABR62590
ABR62590 standard; protein; 651 AA.
XX AC ABR62590;
XX DT 06-NOV-2003 (first entry)
XX DE Anti-CD7 antibody TH-69 scFv-Pseudomonas exotoxin A fusion protein.
XX KM CD7; antibody; TH-69; scFv; exotoxin A; immunotoxin; cytostatic;
XX KW immunosuppressive; vaccine.
XX OS Mus sp.
OS Pseudomonas sp.
OS Synthetic.
OS Chimeric.
XX FT Region
FH Key Location/Qualifiers
FT Region 7..265
FT /label= scFv
FT Region 125..285
FT /label= Linker
FT Region 286..646
FT /label= ETR
XX WO2003051926-A2.
XX PD 26-JUN-2003.
XX PF 11-DEC-2002; 2002WO-BE014064.
XX PR 14-DEC-2001; 2001US-0339422P.

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 7.13276 Seconds
(Without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572
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Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	128	4	US-09-225-322B-10 Sequence 10, Appl
2	572	100.0	128	4	US-09-225-322B-19 Sequence 19, Appl
3	572	100.0	128	4	US-09-764-304-10 Sequence 10, Appl
4	572	100.0	128	4	US-09-764-304-19 Sequence 19, Appl
5	516	90.2	108	3	US-09-065-059-3 Sequence 3, Appl
6	503	87.9	107	2	US-08-652-558-35 Sequence 35, Appl
7	502	87.8	131	1	US-08-236-520-2 Sequence 2, Appl
8	502	87.8	131	5	PCT-US95-05262-2 Sequence 2, Appl
9	498	86.9	112	3	US-08-487-761-13 Sequence 13, Appl
10	497	86.9	109	4	US-09-386-658A-4 Sequence 4, Appl
11	488	85.3	107	1	US-08-458-516-9 Sequence 9, Appl
12	488	85.3	127	1	US-08-458-516-5 Sequence 5, Appl
13	488	85.3	127	3	US-08-649-100-17 Sequence 17, Appl
14	487	85.1	108	3	US-09-199-149-7 Sequence 7, Appl
15	487	85.1	274	4	US-09-813-659-30 Sequence 30, Appl
16	487	85.1	274	4	US-09-549-067A-30 Sequence 30, Appl
17	487	85.1	302	1	US-08-121-054C-18 Sequence 18, Appl
18	487	85.1	302	1	US-08-121-054C-30 Sequence 30, Appl
19	487	85.1	302	3	US-08-539-436-18 Sequence 18, Appl
20	487	85.1	302	3	US-08-539-436-30 Sequence 30, Appl
21	487	85.1	302	4	US-09-813-659-18 Sequence 18, Appl
22	487	85.1	302	4	US-09-813-659-32 Sequence 32, Appl
23	487	85.1	302	4	US-09-549-067A-18 Sequence 18, Appl
24	487	85.1	302	4	US-09-549-067A-32 Sequence 32, Appl
25	484	84.6	109	1	US-07-942-245-10 Sequence 10, Appl
26	483	84.4	107	2	US-07-934-373C-16 Sequence 16, Appl
27	483	84.4	107	3	US-08-437-642B-16 Sequence 16, Appl

28	483	84.4	107	4	US-08-146-206C-16 Sequence 16, Appl
29	483	84.4	107	4	US-09-705-686-16 Sequence 16, Appl
30	483	84.4	107	4	US-09-705-392A-16 Sequence 16, Appl
31	483	84.4	107	5	PCT-US93-07832-16 Sequence 16, Appl
32	483	84.4	127	1	US-08-137-117D-37 Sequence 37, Appl
33	483	84.4	127	2	US-08-436-717-37 Sequence 37, Appl
34	474	82.9	137	1	US-08-137-117D-29 Sequence 29, Appl
35	474	82.9	137	2	US-08-436-717-29 Sequence 29, Appl
36	469	82.0	214	1	US-08-425-763-1 Sequence 1, Appl
37	469	82.0	214	2	US-07-934-373C-24 Sequence 24, Appl
38	469	82.0	214	3	US-08-437-642B-24 Sequence 24, Appl
39	469	82.0	214	3	US-08-811-757-1 Sequence 1, Appl
40	469	82.0	214	3	US-09-249-230-1 Sequence 1, Appl
41	469	82.0	214	4	US-08-146-206C-24 Sequence 24, Appl
42	469	82.0	214	4	US-09-705-686-24 Sequence 24, Appl
43	469	82.0	214	4	US-09-705-392A-24 Sequence 24, Appl
44	469	82.0	214	5	PCT-US93-07832-24 Sequence 24, Appl
45	468	81.8	273	2	US-08-403-853-18 Sequence 18, Appl

ALIGNMENTS

```
RESULT 1
US-09-225-322B-10
; Sequence 10, Application US/09225322B
; Patent No. 6437098
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: HASEGAWA, MAMORU
; APPLICANT: MIYAJI, HIROMASA
; APPLICANT: KOMANA, YOSHITSU
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
; FILE REFERENCE: 249-101
; CURRENT APPLICATION NUMBER: US/09/225,322B
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: US 08/454,680
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/408,133
; PRIOR FILING DATE: 1995-03-21
; PRIOR APPLICATION NUMBER: US 08/292,178
; PRIOR FILING DATE: 1994-08-17
; PRIOR APPLICATION NUMBER: US07/947,674
; PRIOR FILING DATE: 1992-09-17
; PRIOR APPLICATION NUMBER: JP 3-238375
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA KM-641
US-09-225-322B-10
Query Match 100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 DIOMTQTASLPASLDRVTATYFCHQYSLPMTFGGCTLEIKR 60
Db 21 DIOMTQTASLPASLDRVTATYFCHQYSLPMTFGGCTLEIKR 80
Cy 61 RFSGGSGTDTYSLTISNLEPEDATYFCHQYSLPMTFGGCTLEIKR 108
Db 81 RFSGGSGTDTYSLTISNLEPEDATYFCHQYSLPMTFGGCTLEIKR 128
RESULT 2
US-09-225-322B-19
; Sequence 19, Application US/09225322B
```

```
/ Patent No. 6437098
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US 09/225,322B
/ CURRENT FILING DATE: 1999-01-05
/ PRIOR APPLICATION NUMBER: US 08/454,680
/ PRIOR FILING DATE: 1995-05-31
/ PRIOR APPLICATION NUMBER: US 08/408,133
/ PRIOR FILING DATE: 1995-03-21
/ PRIOR APPLICATION NUMBER: US 08/292,178
/ PRIOR FILING DATE: 1994-08-17
/ PRIOR APPLICATION NUMBER: US07/947,674
/ PRIOR FILING DATE: 1992-09-17
/ PRIOR APPLICATION NUMBER: JP 3-238375
/ PRIOR FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:light chain
/ OTHER INFORMATION: variable region
US-09-225-322B-19
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```
Query Match          100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 60
pb 21 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 80
QY 61 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 128
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RESULT 3
US-09-764-304-10
/ Sequence 10, Application US/09764304
/ Patent No. 6495666
/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US 09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
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/ SEQ ID NO 10
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: cDNA KM-641
US-09-764-304-10
```

```
Query Match          100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 60
Db 21 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 80
QY 61 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 128
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RESULT 4
US-09-764-304-19
/ Sequence 19, Application US/09764304
/ Patent No. 6495666
```

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/ GENERAL INFORMATION:
/ APPLICANT: SHITTARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US 09/764,304
/ CURRENT FILING DATE: 2001-01-19
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
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/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
/ OTHER INFORMATION: variable region
US-09-764-304-19
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```
Query Match          100.0%; Score 572; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-51;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 60
Db 21 DIQMTQASLSPASLGDRTVITSCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSHGVS 80
QY 61 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 108
Db 81 RFSGGSGTDYSLTISNLEPEDIAITYFCHQYSKLPMTGGGTYKLEIKR 128
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RESULT 5
US-09-065-059-3
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```

: Sequence 3, Application US/09065059
: Patent No. 6068841
:
: GENERAL INFORMATION:
: APPLICANT: SEINO, Ken-ichi
: APPLICANT: KAVAGAKI, No. 6068841uh1ko
: APPLICANT: YAGITA, Hideo
: APPLICANT: OKUMURA, Ko
: APPLICANT: NAKATA, Motomi
: TITLE OF INVENTION: THERAPEUTIC AGENT FOR HEPATITIS
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDermott, Will & Emery
: STREET: 99 Canal Center Plaza
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22314
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/065, 059
: FILING DATE:
:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Bucca Ph.D., Daniel
: REGISTRATION NUMBER: P-42,368
: REFERENCE/DOCKET NUMBER: 50356-151
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-518-5100
: TELEFAX: 703-684-1124
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 108 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
:
: US-09-065-059-3
:
: Query Match 90.2%; Score 516; DB 3; Length 108;
: Best Local Similarity 89.8%; Pred. No. 1.5e-45;
: Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
:
: QY 1 DIOMQTQSSLPASIGDRVTISCSASODISNLYNMYQOKPDGTVLLIFYSNNLHGVPS 60
: 1 DIOMTQSSSSASASIGDRVTISCRASQDISNLYNMYQOKPDGTVLLIYYSRLHGVPS 60
:
: QY 61 RFGSGGSGTDYSLTISNLEPEDIATYFCHOYSKLPWFEGGKTLEIKR 108
: 61 RFGSGGSGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGKTLEIKR 108
:
: Db 61 RFGSGGSGTDYSLTISNLEPEDIATYFCQYSEFPWTFGGGKTLEIKR 108
:
: RESULT 6
: US-08-652-558-35
: Sequence 35, Application US/08652558
: Patent No. 5861155
:
: GENERAL INFORMATION:
: APPLICANT: LIN, AUGUSTINE YEE-THARN
: TITLE OF INVENTION: HUMANIZED ANTIBODIES AND USES
: TITLE OF INVENTION: THEROP
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER & WITCOFF
: STREET: 75 STATE STREET, 23RD FLOOR
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 02109
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

```

```

      ; OPERATING SYSTEM: PC-DOS/MS-DOS
      ; SOFTWARE: Wordperfect 6.1
      ; CURRENT APPLICATION DATA:
      ; APPLICATION NUMBER: US/08/652,558
      ; FILING DATE: JUNE 6, 1996
      ; PRIOR APPLICATION DATA:
      ; APPLICATION NUMBER: PCT/IB94/00387
      ; FILING DATE: NOVEMBER 21, 1994
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: YANKWICH, LEON R.
      ; REGISTRATION NUMBER: 30,237
      ; REFERENCE/DOCKET NUMBER: 95,497-L
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: 617-345-9100
      ; TELEFAX: 617-345-9111
      ; INFORMATION FOR SEQ ID NO: 35:
      ; SEQUENCE CHARACTERISTICS:
      ; LENGTH: 107 amino acids
      ; TYPE: amino acid
      ; STRANDEDNESS: single
      ; TOPOLOGY: linear
      ; MOLECULE TYPE: protein
      ;
      ; US-08-652-558-35
      ;
      Query Match      87.9%; Score 503; DB 2; Length 107;
      Best Local Similarity 89.7%; Pred. No. 3.2e-44;
      Matches 96; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

      Oy      1 DIOMTQASSLPALIGDVRTTSQASODISNYLNMWYOOKPDGTYKLLIFSSNLHGVPS 60
      Db      1 DIOMTQTTSSLSALSGRVTITSCASGCIISNYLNMWYOOKPDGTYKLLIYTSSLSHGVPS 60
      Oy      61 RFSGSGSGTDYSLTISNLEPEDIAITYECHOYSKLPFTFGGTXYKLEIK 107
      Db      61 RFSGSGSGTDYSLTISNLEPEDIAITYCQGYSKLPFTFGGTXYKLEIK 107

      RESULT 7
      ; US-08-236-520-2
      ; Sequence 2, Application US/08236520
      ; Patent No. 5591629
      ; GENERAL INFORMATION:
      ; APPLICANT: Rodriguez, Moses
      ; APPLICANT: Miller, David J.
      ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
      ; TITLE OF INVENTION: CENTRAL NERVOUS SYSTEM REMYELINATION
      ; NUMBER OF SEQUENCES: 11
      ; CORRESPONDENCE ADDRESS:
      ; ADDRESSEE: Hamilton, Brook, Smithy & Reynolds, P.C.
      ; STREET: Two Millitia Drive
      ; CITY: Lexington
      ; STATE: Massachusetts
      ; COUNTRY: USA
      ; ZIP: 02173
      ;
      ; COMPUTER READABLE FORM:
      ; MEDIUM TYPE: Floppy disk
      ; COMPUTER: IBM PC compatible
      ; OPERATING SYSTEM: PC-DOS/MS-DOS
      ; SOFTWARE: Patentn Release #1.0, Version #1.25
      ; CURRENT APPLICATION DATA:
      ; APPLICATION NUMBER: US/08/236,520
      ; FILING DATE: 29-APR-1994
      ; CLASSIFICATION: 424
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: Granahan, Patricia
      ; REGISTRATION NUMBER: 27,227
      ; REFERENCE/DOCKET NUMBER: MMV92-01
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: 617-861-6240
      ; TELEFAX: 617-861-9540
      ; INFORMATION FOR SEQ ID NO: 2:
      ; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-236-520-2

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Query March	87.8%;	Score 502;	DB 1;	Length 131;
Best Local Similarity	88.9%;	Pred. No. 5.2e-44;		
Matches	96;	Conservative	3;	Mismatches 9;
				Indels 0;
				Gaps 0;

1 DIQMTQTASSLPA SLGDRVTISCSAQDLSINLYNQKKGDTVKLLIFYSNLTGVPSS 600
21 DIQMTQTSSLSASLGDRVTISCPASQDLSINLYNQKKGDTVKLLIYYSRLHGVPS 800

61 RPSGGGSGCTDYSLTISNLEPEDIATYFCHQYSKLPWTFGGGTKLEIKR 108
81 RFGSGSGSDYSLTISNLEQEDIATYFCQGGNTLPWTFGGGTKLEIKR 128

RESULT 8
PCT-US95-05262-2

APPLICANT: Mayo Foundation for Medical Education Research
TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH PROMOTE
ATTACHMENT OF TUMOR-CELLS TO SUBSTRATA

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smyth & Reynolds, P.C.
CMBET, Two Milletts Drive

CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOURCE: CALCULIN ACETABASE #1.0 / VERSION #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05262
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/236,520
FILING DATE: April 29, 1994

NAME: Granahan, Patricia
REGISTRATION NUMBER: 27,227
REFERENCE/DOCKET NUMBER: MMV92-01 PCT

TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:

LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear

Query	Match	87
CT-US95-05262-2		

Matches	96, Conservative	3, Mismatches	9, Indels	0, Gaps
1	DIOMTOTASSLPASIGDRVITISCSAQDISNVLNMYOKKPDGTVKLLIFYSSNIHSGVPS	60		

21 DIQMTQIYSSLSASLGDRVTISCSAQDISNYLNMYQQRKPDGVTKLIYYSRLHSGVPS 80
61 RPSGGSGTDYSLTISNLEPEDIAITYFCHQYSLPWTFFGGTKLEIKR 108

81 KFSGSGSIDVSLISNLEQEDIAITYFCQGNILPWTEGGIKLEIKR 128

RESULT 9
US-08-487-761-13
; Sequence 13, Application US/08487761

```

; GENERAL INFORMATION:
; APPLICANT: Schlössinger, Joseph
; APPLICANT: Givol, David
; ADDRESS: 10101 E. Broadway
;

```

APPLICANT:	Kris, Richard
APPLICANT:	Ricca, George A.
APPLICANT:	Cheadle, Christopher
APPLICANT:	Smith, Victoria J.

;	TITLE OF INVENTION:	Monoclonal
;	TITLE OF INVENTION:	Epidermal G
;	TITLE OF INVENTION:	Employing S
;	NUMBER OF SEQUENCES:	17

CORRESPONDENCE ADDRESS:
ADDRESSEES: Rhone-Poulenc Rorer Inc
STREET: 500 Arcola Road, 3C43
CITY: Collegeville

COUNTRY: USA
ZIP: 19426
COMPUTER READABLE

```

;
;   COMPUTER: Macintosh
;   OPERATING SYSTEM: System
;   SOFTWARE: Word 5.0 (Pater

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APPLICATION NUMBER: US/08/487,761
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

APPLICATION NUMBER: US 08/086,411
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:

```

;
;   REGISTRATION NUMBER: 32,534
;   REFERENCE/DOCKET NUMBER: A0207C-US
;   TELECOMMUNICATION INFORMATION:
;
;   DATE RECEIVED: 04-20-17

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TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
SEQUENCE: 113 amino acids

```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;
TS-08-487-761-13

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Query Match	87.1%;	Score 498;	DB 3;	Length 112
Best Local Similarity	87.0%;	Pred. No. 1.1e-43;		
Matches 94:	Conservative	6;	Mismatches	8; Indels

QY 1 DQMOTASSLPASLGDRVTTSCSASODISNLYLWYQOKPDGTVKLLIFYSNLSHGVP 60

```
QY      61 RFSGGSGSTDYSLTISNLEBEDIATYFCHQYSKLPWTFGGGTKLEIKR   108
        |||||
Db      61 RFSGGSGSTDYSLTISNLEBEDIATYCOOYSKIPTYPTFGGTKLEIKR   108
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RESULT 10
US-09-386-658A-4

Patent No. 6593137
GENERAL INFORMATION:
APPLICANT: Erlanger, Bernard F.

;; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR FULLERENES
; FILE REFERENCE: 0575/54182

;; CURRENT APPLICATION NUMBER: US/09/386,658A
;; CURRENT FILING DATE: 1999-08-31
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 4
;; LENGTH: 109
;; TYPE: PRT
;; ORGANISM: Mouse
US-09-386-658A-4

Query Match 86.9%; Score 497; DB 4; Length 109;
Best Local Similarity 86.1%; Pred. No. 1,3e-43;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 108
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 108

RESULT 11

US-08-458-516-9
;; Sequence 9, Application US/08458516
;; Patent No. 577085
;; GENERAL INFORMATION:
;; APPLICANT: Co, Man Sung
;; APPLICANT: Tso, J. Yun
;; TITLE OF INVENTION: Humanized Antibodies Reactive with
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Stewart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-458-516-9

Query Match 85.3%; Score 488; DB 1; Length 107;
Best Local Similarity 86.9%; Pred. No. 1,1e-42;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60
DB 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60

DB 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 107
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 107

RESULT 12

US-08-458-516-5
;; Sequence 5, Application US/08458516
;; Patent No. 577085
;; GENERAL INFORMATION:
;; APPLICANT: Co, Man Sung
;; APPLICANT: Tso, J. Yun
;; TITLE OF INVENTION: Humanized Antibodies Reactive with
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: William M. Smith
;; STREET: One Market Plaza, Stewart Tower, Suite 2000
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 127 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-458-516-5

Query Match 85.3%; Score 488; DB 1; Length 127;
Best Local Similarity 86.9%; Pred. No. 1,3e-42;
Matches 93; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 60
DB 21 DIQMTQTSSLSASLGRVITSCSASODISNYLWYQKPGDTYKLIIFYSSNLHSGVPS 80

QY 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 107
DB 61 RFSGGSGTDYSLTISNLEPEDIATYFCCHOYSKLPMTFGGDTKLEIKR 107

RESULT 13

US-08-649-100-17
;; Sequence 17, Application US/08649100
;; Patent No. 6114507
;; GENERAL INFORMATION:
;; APPLICANT: SHIRAKAWA, KAMON
;; APPLICANT: MATSUUE, TOMOKAZU
;; APPLICANT: NAGATA, SHIGEKAZU
;; APPLICANT: CO, MAN SUNG

APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,100
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-649-100-17

Query Match 85.3%; Score 488; DB 3; Length 127;
Best Local Similarity 87.9%; Pred. No. 1.3e-42;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASLSPASLGDRTVITSCSASQDISNYLNMYQOKPDGTVKLLIFYSNLSHGVS 60
DB 21 DIQMTQTSSLSASLGDRTVITSCRASQDISNYLNMYQOKPDGTVKLLIYTSRLSHGVS 80
QY 61 RFSGGSGTDVSLTISNLEPEDIAATYFCHQYSKLPWTGGGTRKLEIK 107
DB 81 RFSGGSGTDVSLTISNLEQGDIAATYFCQGGSTLPWTGGGTRKLEIK 127

RESULT 14
US-09-199-149-7
Sequence 7, Application US/09199149
Patent No. 6160099
GENERAL INFORMATION:
APPLICANT: Jonak, Zdenka L.
APPLICANT: Taylor, Alexander H.
APPLICANT: Trulll Jr., Stephen H.
APPLICANT: Johanson, Kyung O.
TITLE OF INVENTION: Humanized Monoclonal Antibodies
FILE REFERENCE: P50860
CURRENT APPLICATION NUMBER: US/09/199,149
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 108
TYPE: PRT
ORGANISM: murine cells
US-09-199-149-7

Query Match 85.1%; Score 487; DB 3; Length 108;
Best Local Similarity 85.2%; Pred. No. 1.4e-42;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQTASLSPASLGDRTVITSCSASQDISNYLNMYQOKPDGTVKLLIFYSNLSHGVS 60
DB 1 DIQMTQTSSLSASLGDRTVITSCRASQDISNYLNMYQOKPDGTVKLLIYTSRLSHGVS 60
QY 61 RFSGGSGTDVSLTISNLEPEDIAATYFCHQYSKLPWTGGGTRKLEIK 108
DB 61 RFSGGSGTDVSLTISNLEQGDIAATYFCQGGSTLPWTGGGTRKLEIK 108

RESULT 15
US-09-813-659-30
Sequence 30, Application US/09813659
Patent No. 6482919
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden, Martha S.
APPLICANT: Linaley, Peter S.
APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, H. Perry
APPLICANT: Gilliland, Lisa K.
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
FILE REFERENCE: 30436.18USD2
CURRENT APPLICATION NUMBER: US/09/813,659
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 09/549,067
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/539,436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-813-659-30

Query Match 85.1%; Score 487; DB 4; Length 274;
Best Local Similarity 85.2%; Pred. No. 4.3e-42;
Matches 92; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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DB 24 DIQMTQTSSLSASLGDRTVITSCRASQDISNYLNMYQOKPDGTVKLLIYTSRLSHGVS 83
QY 61 RFSGGSGTDVSLTISNLEPEDIAATYFCHQYSKLPWTGGGTRKLEIK 108
DB 84 RFSGGSGTDVSLTIANLOPEDIAATYFCQGGSTLPWTGGGTRKLVTKR 131

Search completed: December 23, 2004, 19:08:02
Job time : 8.13276 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 : Search time 24.5684 Seconds
(without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572
Sequence: 1 D1QMGQTASIPASLGDRTV.....HOYSKLPWFEGGSKLEIKR 108

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications AA:*
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20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	572	100.0	128	9	US-09-764-304-10
2	572	100.0	128	9	US-09-764-304-19
3	572	100.0	128	14	US-10-265-713-10
4	572	100.0	128	14	US-10-265-713-19
5	572	100.0	128	14	US-10-166-626-10
6	572	100.0	128	14	US-10-166-626-19
7	510	89.2	108	9	US-09-056-1608-10
8	510	89.2	108	14	US-10-234-671-10
9	502	87.8	131	8	US-08-779-784-21
10	502	87.8	131	14	US-10-010-729-64
11	497	86.9	109	14	US-10-197-080-4
12	494	86.4	107	17	US-10-741-657A-16
13	491	85.8	107	17	US-10-473-977-69

ALIGNMENTS

14	488	85.3	107	15	US-10-411-037-52	Sequence 52, Appl
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16	488	85.3	107	15	US-10-410-963-52	Sequence 52, Appl
17	488	85.3	107	15	US-10-411-049-52	Sequence 52, Appl
18	488	85.3	107	16	US-10-410-930-52	Sequence 52, Appl
19	488	85.3	107	16	US-10-410-997-52	Sequence 52, Appl
20	488	85.3	107	16	US-10-411-012-52	Sequence 52, Appl
21	488	85.3	107	16	US-10-287-994-52	Sequence 52, Appl
22	488	85.3	107	16	US-10-410-913-52	Sequence 52, Appl
23	488	85.3	108	13	US-10-140-555-4	Sequence 4, Appl
24	488	85.3	127	14	US-10-084-139-2	Sequence 2, Appl
25	488	85.3	601	9	US-09-480-236-1	Sequence 1, Appl
26	488	85.3	637	16	US-10-296-085A-16	Sequence 16, Appl
27	488	85.3	638	16	US-10-296-085A-21	Sequence 21, Appl
28	488	85.3	642	16	US-10-296-085A-38	Sequence 38, Appl
29	488	85.3	643	16	US-10-296-085A-69	Sequence 69, Appl
30	488	85.3	656	16	US-10-296-085A-39	Sequence 39, Appl
31	488	85.3	657	16	US-10-296-085A-68	Sequence 68, Appl
32	487	85.1	108	14	US-10-141-908-7	Sequence 7, Appl
33	487	85.1	274	9	US-09-813-659-30	Sequence 30, Appl
34	487	85.1	274	14	US-10-283-610A-30	Sequence 30, Appl
35	487	85.1	302	9	US-09-813-659-18	Sequence 18, Appl
36	487	85.1	302	9	US-09-813-659-32	Sequence 32, Appl
37	487	85.1	302	14	US-10-283-610A-32	Sequence 32, Appl
38	487	85.1	302	14	US-10-283-610A-18	Sequence 18, Appl
39	487	85.1	504	14	US-10-207-655-348	Sequence 348, Appl
40	487	85.1	555	15	US-10-107-991B-3	Sequence 3, Appl
41	485	84.8	107	14	US-10-310-674A-34	Sequence 34, Appl
42	485	84.8	107	15	US-10-389-679-10	Sequence 2, Appl
43	484	84.6	107	14	US-10-269-010-2	Sequence 10, Appl
44	484	84.6	107	14	US-10-268-883-6	Sequence 6, Appl
45	484	84.6	127	14	US-10-268-883-5	Sequence 5, Appl

RESULT 1
US-09-764-304-10
Sequence 10, Application US/09764304
Patent No. US2002026036A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KIWANA, YOSHITHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/09/764,304
EARLIER FILING DATE: 2001-01-19
EARLIER APPLICATION NUMBER: 09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
EARLIER FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CDNA KM-641
US-09-764-304-10

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Query Match          100.0%; Score 572; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTQASLSPASLGDRTVITCSASQDISNYLWYQKRPDGTVKLLIFYSNLSHGVS 60
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Db 21 DIOMTQASLSPASLGDRTVITCSASQDISNYLWYQKRPDGTVKLLIFYSNLSHGVS 80
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Qy 61 RFGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPMTFGGTYKLEIKR 108
    |||
Db 81 RFGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPMTFGGTYKLEIKR 128
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RESULT 2
US-09-764-304-19
/ Sequence 19, Application US/09764304
/ Patent No. US20020026036A1
/ GENERAL INFORMATION:
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA
/ TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
/ FILE REFERENCE: 249-101
/ CURRENT APPLICATION NUMBER: US/09/764,304
/ EARLIER APPLICATION NUMBER: 09/225,322
/ EARLIER FILING DATE: 1999-01-05
/ EARLIER APPLICATION NUMBER: US 08/454,680
/ EARLIER FILING DATE: 1995-05-31
/ EARLIER APPLICATION NUMBER: US 08/408,133
/ EARLIER FILING DATE: 1995-03-21
/ EARLIER APPLICATION NUMBER: US 08/292,178
/ EARLIER FILING DATE: 1994-08-17
/ EARLIER APPLICATION NUMBER: US07/947,674
/ EARLIER FILING DATE: 1992-09-17
/ EARLIER APPLICATION NUMBER: JP 3-238375
/ EARLIER FILING DATE: 1991-09-18
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 128
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: light chain
/ OTHER INFORMATION: variable region
US-09-764-304-19

Query Match          100.0%; Score 572; DB 9; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTQASLSPASLGDRTVITCSASQDISNYLWYQKRPDGTVKLLIFYSNLSHGVS 60
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Db 21 DIOMTQASLSPASLGDRTVITCSASQDISNYLWYQKRPDGTVKLLIFYSNLSHGVS 80
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Qy 61 RFGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPMTFGGTYKLEIKR 108
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Db 81 RFGGSGGTDYSLTISNLEPEDIAFYFCHQYSKLPMTFGGTYKLEIKR 128
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RESULT 3
US-10-265-713-10
/ Sequence 10, Application US/10265713
/ Publication No. US20030095964A1
/ GENERAL INFORMATION:
/ APPLICANT: SHITARA, KENYA
/ APPLICANT: HANAI, NOBUO
/ APPLICANT: HASEGAWA, MAMORU
/ APPLICANT: MIYAJI, HIROMASA
/ APPLICANT: KUMANA, YOSHIHISA

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
EARLIER APPLICATION NUMBER: US/09/225,322
EARLIER FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: US 08/454,680
EARLIER FILING DATE: 1995-05-31
EARLIER APPLICATION NUMBER: US 08/408,133
EARLIER FILING DATE: 1995-03-21
EARLIER APPLICATION NUMBER: US 08/292,178
EARLIER FILING DATE: 1994-08-17
EARLIER APPLICATION NUMBER: US 07/947,674
EARLIER FILING DATE: 1992-09-17
EARLIER APPLICATION NUMBER: JP 3-238375
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: light chain

TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/265,713
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: US/09/225,322
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: light chain
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OTHER INFORMATION: variable region
US-10-265-713-19

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 60
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DB 21 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 80
    |||||||

QY 61 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 108
    |||||||
DB 81 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 128
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RESULT 5
US-10-166-626-10
Sequence 10, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: cDNA KM-641
US-10-166-626-10

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 60
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DB 21 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 80
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QY 61 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 108
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DB 81 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 128
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RESULT 6
US-10-166-626-19
Sequence 19, Application US/10166626
Publication No. US20030166876A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: HASEGAWA, MAMORU
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APPLICANT: MIYAJI, HIROMASA
APPLICANT: KUMANA, YOSHIHISA
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMANIZED CHIMERA ANTIBODY
FILE REFERENCE: 249-101
CURRENT APPLICATION NUMBER: US/10/166,626
PRIOR FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/225,322B
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: US 08/454,680
PRIOR FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/408,133
PRIOR FILING DATE: 1995-03-21
PRIOR APPLICATION NUMBER: US 08/292,178
PRIOR FILING DATE: 1994-08-17
PRIOR APPLICATION NUMBER: US07/947,674
PRIOR FILING DATE: 1992-09-17
PRIOR APPLICATION NUMBER: JP 3-238375
PRIOR FILING DATE: 1991-09-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: light chain
US-10-166-626-19

Query Match      100.0%; Score 572; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 60
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DB 21 D10MTQASLPLASLGRVITSCASQDISNYLWYQOKPDGTVKLLIFYSNLSHGVPS 80
    |||||||

QY 61 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 108
    |||||||
DB 81 RFSGGSGTDYSLTISNLEPEDATYFCHQYSKLPTFGGCTKLEIKR 128
    |||||||

RESULT 7
US-09-056-160B-10
Sequence 10, Application US/09056160B
Patent No. US2002003215A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
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ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-056-160B-10

Query Match 89.2%; Score 510; DB 9; Length 108;
Best Local Similarity 88.0%; Pred. No. 1,6e-39;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASLSPLASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 60
Db 1 DIQMTQTSSLSASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 60

QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTKLEIKR 108
Db 61 RFSGGSGTDYSLTISNLEPEDIAFYCOQYSTVPWTFGGTKLEIKR 108

RESULT 8
US-10-234-671-10
Sequence 10, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid

TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-234-671-10

Query Match 89.2%; Score 510; DB 14; Length 108;
Best Local Similarity 88.0%; Pred. No. 1,6e-39;
Matches 95; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTASLSPLASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 60
Db 1 DIQMTQTSSLSASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 60

QY 61 RFSGGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTKLEIKR 108
Db 61 RFSGGSGTDYSLTISNLEPEDIAFYCOQYSTVPWTFGGTKLEIKR 108

RESULT 9
US-08-779-784-21
Sequence 21, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-784-21

Query Match 87.8%; Score 502; DB 8; Length 131;
Best Local Similarity 88.9%; Pred. No. 1e-38;
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTASLSPLASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 60
Db 21 DIQMTQTSSLSASLDRTVITSCSASQDISNYLNMWYQKRPDGTVKLLIFYSNLSHGVP 80

Qy 61 RFGSGSGTDYSLTISNLEPEDATYFCCHOYSKLPMTFGGTTKLEIKR 108
Db 81 RFGSGSGTDYSLTISNLEPEDATYFCQCGNTLPTMTFGGTTKLEIKR 128

RESULT 10

US-10-010-729-64
Sequence 64, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
FILE REFERENCE: 1199-1-005C1P2
CURRENT APPLICATION NUMBER: US/10/010,729
PRIORITY FILING DATE: 2001-11-13
PRIORITY APPLICATION NUMBER: 09/730,473
PRIORITY FILING DATE: 2000-12-05
PRIORITY APPLICATION NUMBER: 09/580,787
PRIORITY FILING DATE: 2000-05-30
PRIORITY APPLICATION NUMBER: 09/322,862
PRIORITY FILING DATE: 1999-05-28
PRIORITY APPLICATION NUMBER: 08/779,784
PRIORITY FILING DATE: 1997-01-07
PRIORITY APPLICATION NUMBER: 08/692,084
PRIORITY FILING DATE: 1996-08-08
PRIORITY APPLICATION NUMBER: 08/236,520
PRIORITY FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-64

Query Match 87.8%; Score 502; DB 14; Length 131;
Best Local Similarity 88.9%; Pred. No. 1e-38;
Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 60
Db 21 DIQMTQTSSLSASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 80
Qy 61 RFGSGSGTDYSLTISNLEPEDATYFCCHOYSKLPMTFGGTTKLEIKR 108
Db 81 RFGSGSGTDYSLTISNLEPEDATYFCQCGNTLPTMTFGGTTKLEIKR 128

RESULT 11

US-10-197-080-4
Sequence 4, Application US/10197080
Publication No. US20030113940A1
GENERAL INFORMATION:
APPLICANT: Exlanger, Bernard F.
APPLICANT: Sheetz, Michael
APPLICANT: Bruns, Louis
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NANOTUBES AND RELATED METHODS AND COMPOST
FILE REFERENCE: 0575/67096-A
CURRENT APPLICATION NUMBER: US/10/197,080
PRIORITY FILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Mouse
US-10-197-080-4

Query Match 86.9%; Score 497; DB 14; Length 109;
Best Local Similarity 86.1%; Pred. No. 2.5e-38;
Matches 93; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 60
Db 1 DIQMTQTSSLSASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDATYFCCHOYSKLPMTFGGTTKLEIKR 108
Db 61 RFGSGSGTDYSLTISNLEPEDATYFCQCGNTLPTMTFGGTTKLEIKR 108

RESULT 12

US-10-741-657A-16
Sequence 16, Application US/10741657A
Publication No. US20040197325A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs
TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
FILE REFERENCE: 05882.0177.NPUS01
CURRENT APPLICATION NUMBER: US/10/741,657A
PRIORITY FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-10-741-657A-16

Query Match 86.4%; Score 494; DB 17; Length 107;
Best Local Similarity 87.9%; Pred. No. 4.6e-38;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQTASSLPASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 60
Db 1 DIQMTQTSSLSASLGRVTISCSASQDISNYLNMWYQOKPDGVTKLIIFYSSNLSHGVPS 60
Qy 61 RFGSGSGTDYSLTISNLEPEDATYFCCHOYSKLPMTFGGTTKLEIKR 107
Db 61 RFGSGSGTDYSLTISNLEPEDATYFCQCGNTLPTMTFGGTTKLEIKR 107

RESULT 13

US-10-473-977-69
Sequence 69, Application US/10473977
Publication No. US20040253233A1
GENERAL INFORMATION:
APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al
TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND THE USE THEREOF
FILE REFERENCE: 4565-0107P
CURRENT APPLICATION NUMBER: US/10/473,977
PRIORITY FILING DATE: 2003-10-03
PRIORITY APPLICATION NUMBER: PCT/002/00003
PRIORITY FILING DATE: 2002-04-06
PRIORITY APPLICATION NUMBER: CU 84/2001
PRIORITY FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.2
SEQ ID NO 69
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)..(107)
US-10-473-977-69

Query Match 85.8%; Score 491; DB 17; Length 107;
Best Local Similarity 87.9%; Pred. No. 8.8e-38;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03, Search time 5.83589 Seconds

(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-56

Perfect score: 572

Sequence: 1 DDMQTQTASSLPASLGDRVT.....HGYSKLPWTEGGGTLEIKR 108

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	520	90.9	111	2	A38740
2	514	89.9	111	2	E38740
3	510	89.2	111	2	C38740
4	507	88.6	107	2	B49026
5	502	87.8	108	2	S69960
6	502	87.8	111	2	G38740
7	498	87.1	108	1	KVMS73
8	495	86.5	122	2	A29360
9	493	86.2	108	2	S69903
10	489	85.5	115	2	JL0080
11	488	85.3	109	2	KVMSAR
12	488	85.3	109	2	PH0888
13	488	85.3	126	2	A34904
14	485.5	84.9	108	2	S38862
15	485	84.8	128	2	A26406
16	484.5	84.7	107	2	S69901
17	481	84.1	107	2	A48677
18	481	84.1	108	2	S69902
19	480	83.9	108	2	S19970
20	478	83.6	107	2	B48670
21	478	83.6	107	2	B28044
22	475	83.0	107	2	A28044
23	475	83.0	127	2	PH1224
24	474	82.9	107	2	D48677
25	474	82.9	108	2	B26405
26	473	82.7	108	2	PL0282
27	473	82.7	108	2	C26405
28	471.5	82.4	107	2	S69906
29	468	81.8	107	2	S32188

30	466	81.5	105	2	PH0087	Ig kappa chain V r
31	462	80.8	107	2	C48677	Ig light chain V-J
32	461	80.6	108	2	S11124	Ig kappa chain V r
33	447	78.1	108	2	B30551	Ig kappa chain V r
34	429	75.0	115	2	A53276	Ig kappa chain V r
35	426	74.5	108	1	K1HUAU	Ig kappa chain V-I
36	421	73.6	93	2	S38564	Ig kappa chain V r
37	419	73.3	129	2	S52789	Ig kappa chain V r
38	408	71.3	108	1	K1HURE	Ig kappa chain V-I
39	408	71.3	127	2	S40367	Ig kappa chain V-J
40	402	70.3	108	2	B49047	Ig kappa chain V r
41	402	70.3	110	2	S44118	Ig kappa chain V-J
42	400	69.9	108	1	K1HUG	Ig kappa chain V-I
43	399	69.8	108	1	K1HURY	Ig kappa chain V-I
44	399	69.8	131	2	S40352	Ig kappa chain V-I
45	396	69.2	108	2	S19674	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A38740

Ig kappa chain V region (Py20) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004

C/Accession: A38740

R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991

A>Title: Heavy and light chain variable region sequences and antibody properties of ant

A/Reference number: A38740; PMID:1177923; PMID:1106720

A/Accession: A38740

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A/Residues: 1-111 <RUF>

A/Molecule type: mRNA

A/Cross-references: UNIPROT:Q91WS9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 90.9%; Score 520; DB 2; Length 111;

Best Local Similarity 88.9%; Pred. No. 1.1e-40;

Matches 96; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDMQTQTASSLPASLGDRVTSCSAGQDISNYINMTQKPDGTVKLIIFYSNLSGVPs 60

DB 4 DDMQTQTASSLPASLGDRVTSCSAGQDISNYINMTQKPDGTVKLIIFYSNLSGVPs 63

QY 61 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGCTLEIKR 108

DB 64 RFGSGSGTDYSLTISNLEPEDATYFCHQYSKLPMTFGGCTLEIKR 111

RESULT 2
E38740
Ig kappa chain V region (Py54) - mouse
C:Species: Mus musculus (house mouse)
C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C/Accession: E38740
R/Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A>Title: Heavy and light chain variable region sequences and antibody properties of ant
A/Reference number: A38740; PMID:1177923; PMID:1106720
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A/Molecule type: mRNA
A/Residues: 1-111 <RUF>
A/Cross-references: UNIPROT:Q91WS9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 89.9%; Score 514; DB 2; Length 111;

RESULT 15

A26406
 Ig kappa chain V region (Ara-A) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
 C/Accession: A26406
 R/Sanz, I.; Capra, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987
 A/Title: V-K and J-K gene segments of A/J Ara-A antibodies: somatic recombination genera
 A/Reference number: A26406; MUID:87147197; PMID:3103124
 A/Accession: A26406
 A/Molecule type: DNA
 A/Residues: 1-128 <SAN>
 A/Cross-references: UNIPROT:Q91WF8; GB:M15519
 C/Superfamily: immunoglobulin V region; immunoglobulin
 C/Keywords: heterotrimer; immunoglobulin
 F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 485; DB 2; Length 128;
 Best Local Similarity 87.0%; Pred. No. 2e-37;
 Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQWTQTASSLPASLGDRTISCSASQDISNYLNMWYQOKPDGTVKLLIFYSNLSGVPS 60
 |||||
 Db 21 DIQWTQTSSLSASLGDRTISCRASQDISNYLNMWYQOKPDGTVKLLIYTSRLHSGVPS 80
 |||||
 QY 61 RFGSGGSGTDYSLTISNLEPEDLATYFCHQYSKLPMTFGGGTKLEIKR 108
 |||||
 Db 81 RFGSGGSGTDYSLTISNLEQEDISTYFCQOGNALPRTFGGGTKLEIKR 128
 |||||

Search completed: December 23, 2004, 19:06:06
 Job time : 5.83589 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 30.044 Seconds

(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-56
Perfect score: 572
Sequence: 1 DQMGTQASLPSLGDRTV.....HOYSKLPWTRGGTKLEIKR 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Filtering filter 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	88.5	233	2 Q91WS9	Q91WS9 mus musculu
2	498	87.1	108	1 KVSJ MOUSE	P01643 mus musculu
3	494	86.4	234	2 Q8R062	Q8R062 mus musculu
4	489	85.5	108	1 KVSJ MOUSE	P01644 mus musculu
5	488	85.3	108	1 KVSJ MOUSE	P01645 mus musculu
6	486	85.0	111	2 AAR10992	AAR10992 mus muscu
7	484	84.6	108	1 KVSJ MOUSE	P01647 mus musculu
8	481	84.1	108	1 KVSJ MOUSE	P01646 mus musculu
9	477	83.4	108	1 KVSJ MOUSE	P01648 mus musculu
10	466	81.5	234	2 Q91WS9	Q91WS9 mus musculu
11	460	80.4	107	2 Q91WS9	Q91WS9 mus musculu
12	458	80.1	108	1 KVSJ MOUSE	P01646 mus musculu
13	457	79.9	103	2 AAR1052	AAR1052 mus muscu
14	437	76.4	104	2 AAR1043	AAR1043 mus muscu
15	436	76.2	104	2 AAR1000	AAR1000 mus muscu
16	426	74.5	108	1 KVSJ MOUSE	P01647 mus musculu
17	408	71.3	108	1 KVSJ MOUSE	P01648 mus musculu
18	401	70.1	108	1 KVSJ MOUSE	P01649 mus musculu
19	400	69.9	108	1 KVSJ MOUSE	P01650 mus musculu
20	399	69.8	108	1 KVSJ MOUSE	P01651 mus musculu
21	396	69.2	108	2 Q91WS9	Q91WS9 mus musculu
22	394.5	69.0	107	2 Q91WS9	Q91WS9 mus musculu
23	394	68.9	108	1 KVSJ MOUSE	P01649 mus musculu
24	394	68.9	108	1 KVSJ MOUSE	P01650 mus musculu
25	394	68.9	236	2 Q6GMX0	Q6GMX0 mus musculu
26	386	67.3	236	2 Q6GMX0	Q6GMX0 mus musculu
27	385	67.3	108	1 KVSJ MOUSE	P01651 mus musculu
28	385	67.3	236	2 Q6GMX0	Q6GMX0 mus musculu
29	383	67.0	108	1 KVSJ MOUSE	P01652 mus musculu
30	382	66.8	236	2 Q6GMX0	Q6GMX0 mus musculu
31	380	66.4	108	1 KVSJ MOUSE	P01653 mus musculu

32	380	66.4	236	2 Q7TMK3	Q7TMK3 mus musculu
33	379	66.3	236	2 Q6GMX8	Q6GMX8 mus musculu
34	377	65.9	108	1 KVSJ MOUSE	P01649 mus musculu
35	375	65.6	116	2 Q96FF6	Q96FF6 mus musculu
36	375	65.6	236	2 Q6PIH7	Q6PIH7 mus musculu
37	375	65.6	236	2 AAR34141	AAR34141 mus musculu
38	374	65.4	108	1 KVSJ MOUSE	P01650 mus musculu
39	374	65.4	108	1 KVSJ MOUSE	P01651 mus musculu
40	374	65.4	108	1 KVSJ MOUSE	P01652 mus musculu
41	374	65.4	129	1 KVSJ MOUSE	P01653 mus musculu
42	371.5	64.9	107	2 Q91WS9	Q91WS9 mus musculu
43	370	64.7	108	1 KVSJ MOUSE	P01654 mus musculu
44	370	64.7	108	1 KVSJ MOUSE	P01655 mus musculu
45	370	64.7	236	2 Q7TS98	Q7TS98 mus musculu

ALIGNMENTS

RESULT 1
Q91WS9 PRELIMINARY, PRT, 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
RA Datchenko L., Matulis K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueffing T.B., Tothiyuk S., Carninci P., Prange C.,
RA Raha S.S., Lottelmeier N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettner M., Madan A., Young A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravynetski M.I., Skalska U., Smalins D.E., Schmeckel A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013496; AAL13496.1; -.
DR PIR: A38740; A38740.
DR PIR: C38740; C38740.
DR PIR: E38740; E38740.
DR PIR: G38740; G38740.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; Cl-sec; 1.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_Like; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 88.5%; Score 506; DB 2; Length 233;
Best Local Similarity 88.0%; Pred. No. 2,4e-43;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQTASLPSASLGDRTYISCSASODISNYLNMYQOKPDDGTVKLLIFYSNLSHGVS 60
DB 20 DIQMTQTSSLSASLGDRTYISCSGSGQGIANYLNMYQOKPDDGTVKLLIYTTSSLSHGVS 79

QY 61 RFSGGSGGTGYSLTISNLEPEDYATYFCHQYSKLPMTFGGTYKLEIKR 108
DB 80 RFSGGSGGTGYSLTISNLEPEDYATYCOQYRILPMTFGGTYKLEIKR 127

RESULT 2

KVSJ MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=76091934; Pubmed=812696;

RA Schiff C., Fougereau M.,
RT "Determination of the primary structure of a mouse IgG2a
immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.

DR HSSP; P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 87.1%; Score 498; DB 1; Length 108;
Best Local Similarity 85.2%; Pred. No. 6,6e-43;
Matches 92; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTASLPSASLGDRTYISCSASODISNYLNMYQOKPDDGTVKLLIFYSNLSHGVS 60
DB 1 DIQMTQTSSLSASLGDRTYISCSASQSIGIANYLNMYQOKPDDGTVKLLIYTTSSLSHGVS 60

QY 61 RFSGGSGGTGYSLTISNLEPEDYATYFCHQYSKLPMTFGGTYKLEIKR 108
DB 61 RFSGGSGGTGYSLTISNLEPEDYATYCOQYSKLPMTFGGTYKLEIKR 108

RESULT 3
Q8R062 PRELIMINARY; PRT; 234 AA.

AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon; PubMed=12477932;
MEDLINE=22388257; Pubmed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Kang U., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Sanchez A.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027418; AAH27418.1; -.
DR HSSP; P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25858 MW; 4EB08C91426AEAB1 CRC64;

Query Match 86.4%; Score 494; DB 2; Length 234;
Best Local Similarity 87.0%; Pred. No. 4,1e-42;
Matches 94; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQTASLPSASLGDRTYISCSASODISNYLNMYQOKPDDGTVKLLIFYSNLSHGVS 60
DB 21 DIQMTQTSSLSASLGDRTYISCSASQSIGIANYLNMYQOKPDDGTVKLLIYTTSSLSHGVS 80

QY 61 RFSGGSGGTGYSLTISNLEPEDYATYFCHQYSKLPMTFGGTYKLEIKR 108
DB 81 RFSGGSGGTGYSLTISNLEPEDYATYCOQYSQPFPTGSGTYKLEIKR 128

RESULT 4
KVSJ MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig kappa chain V-V region HP R16.7.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR PIR; A01927; KVMAR.
 DR HSSP; P01594; IUV5.
 DR Interpro; IPR007110; Ig_1like.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 108 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 85.5%; Score 489; DB 1; Length 108;
 Best Local Similarity 88.0%; Pred. No. 5.4e-42;
 Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQASLPSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIFYSNLSHGVS 60
 DB 1 DIQMTQTSLSLSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIYTSRLHSGVPS 60
 QY 61 RFGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 108
 DB 61 RFGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 108

RESULT 5

KVSL_MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSSP; P01607; IREI.
 DR Interpro; IPR007110; Ig_1like.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.

DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 108 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 85.3%; Score 489; DB 1; Length 108;
 Best Local Similarity 88.0%; Pred. No. 6.9e-42;
 Matches 95; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQASLPSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIFYSNLSHGVS 60
 DB 1 DIQMTQTSLSLSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIYTSRLHSGVPS 60
 QY 61 RFGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 108
 DB 61 RFGSGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 108

RESULT 6

AARI0992 PRELIMINARY; PRT; 111 AA.
 ID AARI0992;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY36832; AARI0992.1; -.
 FT NON TER 1
 FT NON TER 111
 SQ SEQUENCE 111 AA; 12120 MW; 879A9D6B5880C59D CRC64;

Query Match 85.0%; Score 486; DB 2; Length 111;
 Best Local Similarity 88.6%; Pred. No. 1.1e-41;
 Matches 93; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 MTQTASLPSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIFYSNLSHGVS 63
 DB 1 MTQTSSLSLSLSDRVITISCSASQDISNYLNMWYQOKPDGVKLLIYTSRLHSGVPS 60
 QY 64 GGGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 108
 DB 61 GGGSGTDYSLTISNLEPEDVATYFCHQYSKLPWTFGGGTLEIKR 105

RESULT 7

KVSN_MOUSE STANDARD; PRT; 108 AA.
 ID KVSN_MOUSE
 AC P01647;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-V region HP 124E1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RA MEDLINE=82150934; PubMed=6801658;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP: P01607; IRI.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653BFEEA2 CRC64;

Query Match
Best Local Similarity 84.6%; Score 484; DB 1; Length 108;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMOTASSLPASIGDRVTISCSASODISNYLNMWYQOKPDGTVLLIFYSNLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMOTSSLSASIGDRVTISCRASQDINNINLMWYQOKPDGTVLLIYTSRLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDVSLTISNLEPEDIAITYFCHQYSKLPWTFGGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGTDVSLTISNLEPEDIAITYFCQGGKLPRTFGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
KV50 MOUSE STANDARD; PRT; 108 AA.
ID KV50_MOUSE
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=82150934; PubMed=6801658;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP: P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;

Query Match
Best Local Similarity 83.4%; Score 477; DB 1; Length 108;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
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FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match
Best Local Similarity 84.1%; Score 481; DB 1; Length 108;
Matches 94; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMOTASSLPASIGDRVTISCSASODISNYLNMWYQOKPDGTVLLIFYSNLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMOTSSLSASIGDRVTISCRASQDINNINLMWYQOKPDGTVLLIYTSRLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDVSLTISNLEPEDIAITYFCHQYSKLPWTFGGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGTDVSLTISNLEPEDIAITYFCQGGYLPRTFGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
KV50 MOUSE STANDARD; PRT; 108 AA.
ID KV50_MOUSE
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=82150934; PubMed=6801658;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP: P01594; IJVS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5B9A45291C CRC64;

Query Match
Best Local Similarity 85.2%; Score 477; DB 1; Length 108;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMOTASSLPASIGDRVTISCSASODISNYLNMWYQOKPDGTVLLIFYSNLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIQMOTSSLSASIGDRVTISCRASQDINNINLMWYQOKPDGTVLLIYTSRLSHGVS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 RFGSGSGTDVSLTISNLEPEDIAITYFCHQYSKLPWTFGGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RFGSGSGTDVSLTISNLEPEDIAITYFCQGGYLPRTFGGTYKLEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 10

091WF8 PRELIMINARY; PRT; 234 AA.

ID 091WF8

AC 091WF8

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien P., Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Plange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fehy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dixon M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kravinsky M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RX STRAUSBERG R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC015292; AAI15292.1; -.

DR PIR: A26406; A26406.

DR PIR: A34904; A34904.

DR PDB: 1JFQ; X-ray; L=21-234.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003597; IG-cl.

DR InterPro: IPR003006; IG_MHC.

DR InterPro: IPR003596; IG_V.

DR InterPro: IPR001865; Ribosomal_S2.

DR Pfam: PF07654; Cl-sec; 1.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

DR PROSITE: PSS0835; IG-LIKE; 2.

DR PROSITE: PSS00290; IG_MHC; UNKNOWN_1.

DR PROSITE: PSS00962; RIBOSOMAL_S2_1; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 234 AA; 25929 MW; B0D08E6B7812D2 CRC64;

Query Match 81.5%; Score 466; DB 2; Length 234;

Best Local Similarity 83.3%; Pred. No. 2.9e-39;

Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIOMTQTASLSPASLDGRVTISCSASQDISNYLWYQKRGDTVKLIIFYSNLSHGVS 60

DB 21 DIOMTQTSSLSASLDGRVTISCRASQDISNYLWYQKRGDTVKLIIFYSNLSHGVS 80

QY 61 RFGSGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTGLKLEIKR 108

DB 81 RFGSGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTGLKLEIKR 128

RESULT 11

09JUL84 PRELIMINARY; PRT; 107 AA.

ID 09JUL84

AC 09JUL84

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Anti-myosin immunoglobulin light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BA1B/C;

RX MEDLINE=20448942; PubMed=10992488;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RT "T-cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL: AF206022; AAF69320.1; -.

DR HSSP: P01594; 1JVS.

DR InterPro: IPR007110; IG-like.

DR InterPro: IPR003596; IG_V.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IgV; 1.

DR PROSITE: PSS0835; IG-LIKE; 1.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 107 AA; 11648 MW; ACF9B1253ACA15SD CRC64;

Query Match 80.4%; Score 460; DB 2; Length 107;

Best Local Similarity 81.3%; Pred. No. 4.9e-39;

Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIOMTQTASLSPASLDGRVTISCSASQDISNYLWYQKRGDTVKLIIFYSNLSHGVS 60

DB 1 DIOMTQTSSLSASLDGRVTISCRASQDISNYLWYQKRGDTVKLIIFYSNLSHGVS 60

QY 61 RFGSGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTGLKLEIKR 107

DB 61 RFGSGSGTDYSLTISNLEPEDIAFYCHQYSKLPWTFGGTGLKLEIKR 107

RESULT 12

KVSU_MOUSE STANDARD; PRT; 108 AA.

ID KVSU_MOUSE

AC P04946;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 29-MAR-2004 (Rel. 43, Last annotation update)

DE Ig kappa chain V-V region NOS-89.4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=63271467; PubMed=6877353;

RX Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

RT "RNA sequences define an unusually restricted Igg response to 2-phenylloxazalone and its early diversification."

RL Nature 304:320-324(1983).

CC -1- FUNCTION: Anti-2-phenyl oxazolone (PROX) Antibody.

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entitles requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; K00745; AAA38690.1; -.
DR HSRP; P01594; IUV5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11866 MW; DB2C85920DC6DD CRC64;

Query Match 80.1%; Score 458; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 7, 8e-39;
Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DQMTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 60
DB 1 DQMTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 60
QY 61 RSGSGGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 108
DB 61 RSGSGGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 108

RESULT 13
AAR11052 PRELIMINARY; PRT; 103 AA.

AC AAR11052;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436892; AAR11052.1; -.
FT NON TER 1 1
FT NON TER 103 103
SQ SEQUENCE 103 AA; 11332 MW; B103B7D98711B901 CRC64;

Query Match 79.9%; Score 457; DB 2; Length 103;
Best Local Similarity 86.3%; Pred. No. 9, 4e-39;
Matches 88; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 4 MQTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 63
DB 1 MQTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 60
QY 64 GSGSGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 105
DB 61 GSGSGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 102

RESULT 14
AAR11043

ID AAR11043 PRELIMINARY; PRT; 104 AA.

AC AAR11043;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436883; AAR11043.1; -.
FT NON TER 1 1
FT NON TER 104 104
SQ SEQUENCE 104 AA; 11473 MW; 5BE393C037D426A7 CRC64;

Query Match 76.4%; Score 437; DB 2; Length 104;
Best Local Similarity 82.8%; Pred. No. 1e-36;
Matches 82; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 MQTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 63
DB 1 MQTASLPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPS 60
QY 64 GSGSGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGK 102
DB 61 GSGSGTGYSLTISNLEPEDIAITYFCHQYSKLPWTFGGK 99

RESULT 15
AAR11000 PRELIMINARY; PRT; 104 AA.

AC AAR11000;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436840; AAR11000.1; -.
FT NON TER 1 1
FT NON TER 104 104
SQ SEQUENCE 104 AA; 11250 MW; 014C270D5B104DC6 CRC64;

Query Match 76.2%; Score 436; DB 2; Length 104;
Best Local Similarity 83.7%; Pred. No. 1, 3e-36;
Matches 82; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 11 LPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPSRSGSGGTD 70
DB 1 LPASLGRVTISCSASODISNYLNMWQOKPDGTVLLIFYSNLHSGVPSRSGSGGTD 60
QY 71 YSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 108
DB 61 YSLTISNLEPEDIAITYFCHQYSKLPWTFGGKLEIKR 98

Search completed: December 23, 2004, 19:04:40
Job time : 31.044 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:30:04 ; Search time 155.692 Seconds
(without alignments)
1340.986 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071
Sequence: 1 EVTVSSGGDFVKGGSGLKV.....IVEFLNRWTFQGSIIITLRL 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residue

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3071	100.0	582	4 AAB81991	Aab81991 Gangliosid
2	3026	98.5	582	4 AAB81987	Aab81987 Gangliosid
3	2759.5	89.9	583	4 AAB83156	Aab83156 Gangliosid
4	2744.5	89.4	579	6 AAB83444	Aab83444 KS antibo
5	2738.5	89.2	579	6 AAO30910	Aao30910 di-KS-ala
6	2731.5	88.9	581	4 AAB81972	Aab81972 Gangliosid
7	2715.5	88.4	575	8 ADP42961	Adp42961 Humanised
8	2592	84.4	580	6 AAO30915	Aao30915 di-NHS76
9	2560	83.4	580	6 AAO30913	Aao30913 di-NHS76
10	2218.5	72.2	449	5 AAO18400	Aao18400 Mature hu
11	2216	72.2	713	8 ADN97491	Adn97491 Artificial
12	2216	72.2	715	8 ADN97489	Adn97489 Artificial
13	2209.5	71.9	475	7 ADMA7075	Adma7075 Mouse ant
14	2205	71.8	477	2 AAR47453	Aar47453 chIT84.12
15	2203.5	71.8	471	8 ADM72029	Adm72029 Chimeric
16	2201.5	71.7	447	6 AAB83522	Aab83522 Human AOC
17	2200.5	71.7	444	6 AAB83527	Aab83527 Humanised
18	2200.5	71.7	444	6 AAB83527	Aab83527 Humanised
19	2200.5	71.7	444	8 ADL15443	Adl15443 Humanised
20	2200.5	71.7	444	8 ADL15443	Adl15443 Humanised
21	2195.5	71.5	445	6 ADO00851	Ado00851 Humanised
22	2195.5	71.5	447	6 AAB33523	Aab33523 Human A2-
23	2194.5	71.5	450	6 AAB34587	Aab34587 023 heavy
24	2194	71.4	449	6 ABP58273	Abp58273 Humanised
25	2194	71.4	468	6 ABP58275	Abp58275 Humanised

26	2191.5	71.4	447	6 AAE33524	Aae33524 Human AOC
27	2189.5	71.3	463	8 ADM72025	Adm72025 Chimeric
28	2187	71.2	451	8 ADH34584	Adh34584 008 heavy
29	2184.5	71.1	446	7 ADF11425	Adf11425 208 anti-
30	2184	71.1	451	8 ADP88494	Adp88494 Humanised
31	2181	71.0	449	3 AAY68810	Aay68810 A rat hea
32	2181	71.0	474	5 AAO14065	Aao14065 Heavy cha
33	2181	71.0	474	6 ABU08017	Abu08017 Human mon
34	2181	71.0	474	7 ADE65775	Ad65775 Human mon
35	2181	71.0	474	8 ADJ92515	Adj92515 Human SOV
36	2180.5	71.0	461	6 ABR39847	Ab39847 Hu266 N56
37	2180.5	71.0	461	6 ABR39843	Ab39843 Hu266 N56
38	2177.5	70.9	442	6 ABR39465	Ab39465 Humanised
39	2177.5	70.9	442	6 ABU08311	Abu08311 Humanised
40	2177.5	70.9	442	6 ABB80109	Abb80109 Heavy, cha
41	2177.5	70.9	442	7 ADE94066	Ad94066 Humanised
42	2177.5	70.9	442	8 ADN61714	Adn61714 Humanised
43	2177.5	70.9	461	4 AAU07745	Aau07745 Humanised
44	2177.5	70.9	461	6 ABR39844	Ab39844 Hu266 N56
45	2177.5	70.9	461	6 ABR39848	Ab39848 Hu266 N56

ALIGNMENTS

RESULT 1
AAB81991
ID AAB81991 standard; protein; 582 AA.
XX
AC AAB81991;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 57.
XX
KM Ganglioside; GD3; complementarity determining region; CDR; antibody;
KW cancer.
XX
OS Synthetic.
XX
PN WO200123432-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-DP06774.
XX
PR 30-SEP-1999; 99JP-00278291.
PR 06-APR-2000; 2000JP-00105086.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266143/27.
XX
PT New human type complementation-determining region-transplanted antibody
PT and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT of e.g. tumors, with low antigenicity, little side effects but potent
PT activity in cancer.
XX
PS Claim 39; Page 175-179; 183pp; Japanese.
XX
CC The present invention describes a monoclonal antibody which can react
CC specifically with ganglioside GD3. The antibody and its derivatives are
CC useful in the diagnosis and therapy of tumours, particularly cancer
CC diagnosis. The present sequence is a protein used in the exemplification
CC of the invention
XX
SQ Sequence 582 AA;
XX
Query Match 100.0%; Score 3071; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 EYTLVESGGD FVYKPGGSLKVCASGFAFSHYAMSVNRQTPAKRLEWVA YISSGSGSTYY 60
DB      1 EYTLVESGGD FVYKPGGSLKVCASGFAFSHYAMSVNRQTPAKRLEWVA YISSGSGSTYY 60
QY      61 SDSVKG RFTISRDN AKNTLYLQMRSLRSDSAMYFC TRVYKLGTYYPDSWGQGTTLTVSSA 120
DB      61 SDSVKG RFTISRDN AKNTLYLQMRSLRSDSAMYFC TRVYKLGTYYPDSWGQGTTLTVSSA 120
QY      121 STKGPSVFPFLAPSSKSTSGGTAALGCLVNDYPRPEVTVMNSGALTSGVHTTTPAVLQSSG 180
DB      121 STKGPSVFPFLAPSSKSTSGGTAALGCLVNDYPRPEVTVMNSGALTSGVHTTTPAVLQSSG 180
QY      181 LYSLSGVTVVPSSSLGTQTYICNVNHPKPNNTKVDKKEBKS CDKHTTCCPCAPELLGCP 240
DB      181 LYSLSGVTVVPSSSLGTQTYICNVNHPKPNNTKVDKKEBKS CDKHTTCCPCAPELLGCP 240
QY      241 SVFLPFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKRREQYNS 300
DB      241 SVFLPFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKRREQYNS 300
QY      301 TYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
DB      301 TYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
QY      361 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMQ 420
DB      361 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMQ 420
QY      421 QGNVPSCSVMHEALNNHYTQKSLISPGKAPTSSTSTKKTQLQLEHLLDLQMLINGINNY 480
DB      421 QGNVPSCSVMHEALNNHYTQKSLISPGKAPTSSTSTKKTQLQLEHLLDLQMLINGINNY 480
QY      481 KNPKLT RMLTFK FVMPK KATELKHLCLEBEELKPLEEVNLT AQSKNFHLRPDLISNINV 540
DB      481 KNPKLT RMLTFK FVMPK KATELKHLCLEBEELKPLEEVNLT AQSKNFHLRPDLISNINV 540
QY      541 IYVLELKGSETTFMCEYADETATIV EFLNRWITFCQSIISTLT 582
DB      541 IYVLELKGSETTFMCEYADETATIV EFLNRWITFCQSIISTLT 582

RESULT 2
AAB81987
ID      AAB81987 standard; protein; 582 AA.
XX
AC      AAB81987;
XX
DT      03-JUL-2001 (first entry)
XX
DE      Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.
XX
KM      Ganglioside; GD3; complementarity determining region; CDR; antibody;
XX      cancer.
XX
OS      Synthetic.
XX
PN      WO200123432-A1.
XX
PD      05-APR-2001.
XX
PF      29-SEP-2000; 2000WO-JP006774.
XX
PR      30-SEP-1999; 99JP-00278291.
XX
PR      06-APR-2000; 2000JP-00105088.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR      WPI; 2001-266143/27.
XX
PT      New human type complementation-determining region-transplanted antibody

```

```

PT      and derivatives against ganglioside GD3, useful in diagnosis and therapy
PT      of e.g. tumors, with low antigenicity, little side effects but potent
PT      activity in cancer.
XX
PS      Claim 41; Page 168-172; 183pp; Japanese.
XX
CC      The present invention describes a monoclonal antibody which can react
CC      specifically with ganglioside GD3. The antibody and its derivatives are
CC      useful in the diagnosis and therapy of tumors, particularly cancer
CC      diagnosis. The present sequence is a protein used in the exemplification
CC      of the invention
XX
SQ      Sequence 582 AA;
XX
Query Match      98.5%; Score 3026; DB 4; Length 582;
Best Local Similarity 98.3%; Pred No. 8.7e-147;
Matches 512; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY      1 EYTLVESGGD FVYKPGGSLKVCASGFAFSHYAMSVNRQTPAKRLEWVA YISSGSGSTYY 60
DB      1 EYTLVESGGD FVYKPGGSLKVCASGFAFSHYAMSVNRQTPAKRLEWVA YISSGSGSTYY 60
QY      61 SDSVKG RFTISRDN AKNTLYLQMRSLRSDSAMYFC TRVYKLGTYYPDSWGQGTTLTVSSA 120
DB      61 SDSVKG RFTISRDN AKNTLYLQMRSLRSDSAMYFC TRVYKLGTYYPDSWGQGTTLTVSSA 120
QY      121 STKGPSVFPFLAPSSKSTSGGTAALGCLVNDYPRPEVTVMNSGALTSGVHTTTPAVLQSSG 180
DB      121 STKGPSVFPFLAPSSKSTSGGTAALGCLVNDYPRPEVTVMNSGALTSGVHTTTPAVLQSSG 180
QY      181 LYSLSGVTVVPSSSLGTQTYICNVNHPKPNNTKVDKKEBKS CDKHTTCCPCAPELLGCP 240
DB      181 LYSLSGVTVVPSSSLGTQTYICNVNHPKPNNTKVDKKEBKS CDKHTTCCPCAPELLGCP 240
QY      241 SVFLPFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKRREQYNS 300
DB      241 SVFLPFPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFMNYVDGVEVNAKTKRREQYNS 300
QY      301 TYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
DB      301 TYRVSVLTVLHODMNLNGEKYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDEL 360
QY      361 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMQ 420
DB      361 TKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMQ 420
QY      421 QGNVPSCSVMHEALNNHYTQKSLISPGKAPTSSTSTKKTQLQLEHLLDLQMLINGINNY 480
DB      421 QGNVPSCSVMHEALNNHYTQKSLISPGKAPTSSTSTKKTQLQLEHLLDLQMLINGINNY 480
QY      481 KNPKLT RMLTFK FVMPK KATELKHLCLEBEELKPLEEVNLT AQSKNFHLRPDLISNINV 540
DB      481 KNPKLT RMLTFK FVMPK KATELKHLCLEBEELKPLEEVNLT AQSKNFHLRPDLISNINV 540
QY      541 IYVLELKGSETTFMCEYADETATIV EFLNRWITFCQSIISTLT 582
DB      541 IYVLELKGSETTFMCEYADETATIV EFLNRWITFCQSIISTLT 582

RESULT 3
AAB83156
ID      AAB83156 standard; protein; 583 AA.
XX
AC      AAB83156;
XX
DT      02-JUL-2001 (first entry)
XX
DE      Ganglioside GM2 antibody-related protein #1.
XX
KM      Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.
XX
OS      Unidentified.
XX

```

Query Match	89.9%; Score 2759.5; DB 4; Length 583;
Beat Local Similarity	89.4%; Pred. No. 3.6e-133;
Matches 523; Conservative 21; Mismatches 36; Indels 5; Gaps 2;	
1 EVTLVESGDFYKPGSLKLVSCAGAFAPSHYMSWVQTPAKRLMEVAYISSGSGSTYY	60
1 EVQLVQSAEYVKRPPASVSKASGKSGYFTDNDMDVKSPOQGLEMGYIYPNNGGTGY	60
61 SDSVYGRFTTIRDNKNTLYLOMRSLRSEDSAMVFCRKYLGTY---FDSMGQSTLT	117
61 NQKFSKATITTDISTSTAYMELHLSREDDAVYIC--ATYGHYGYMFAYMGQSTLT	118
118 SSASTKGPVPEPLAPSSKSTSGTAALCLVVDYFPEBVTVSMNSGALTSGVHTP	177
119 SSASTKGPVPEPLAPSSKSTSGTAALCLVVDYFPEBVTVSMNSGALTSGVHTP	178
178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKVBEKSCDKTHTCP	237
179 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKVBEKSCDKTHTCP	238
238 GGPVSFELPPPKDQTLMTSRPEVYCVVVDVSHEDPEKFMVYVNDGVVNAKTKR	297
239 GGPVSFELPPPKDQTLMTSRPEVYCVVVDVSHEDPEKFMVYVNDGVVNAKTKR	298
298 YNSTYRVSVLTVLHQDMLNGEKYCKYSNNKALPAPIEKTISKAKGQPREPOVY	357
299 YNSTYRVSVLTVLHQDMLNGEKYCKYSNNKALPAPIEKTISKAKGQPREPOVY	358
358 DELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPYLVDGSGFFLYSK	417
359 DELTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPYLVDGSGFFLYSK	418
418 RMQGNVSSCSVMHEALNHTQKSLSPGAPRPSSTTKTQLOLEHLLDLQMTLNGI	477
419 RMQGNVSSCSVMHEALNHTQKSLSPGAPRPSSTTKTQLOLEHLLDLQMTLNGI	478
478 NNYKPKPLTRMLTFEYMPKATBELKHLQCLEEELKPLEEVLNLAQSNFLRPDLIS	537
479 NNYKPKPLTRMLTFEYMPKATBELKHLQCLEEELKPLEEVLNLAQSNFLRPDLIS	538
538 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT	582
539 INVIVLELKGSETTFMCEYADETATVEFLNRWITFCOSIISTLT	583

ID	AAE33444	standard; protein; 579 AA.
XX		
AC	AAE33444;	
XX		
DT	02-APR-2003	(first entry)
XX		
DE	KS antibody heavy chain-interleukin 2 (IL-2) fusion protein.	
XX		
KW	Immunoglobulin; diagnosis; epithelial cell adhesion molecule; EpCAM;	
KW	cancer; gene therapy; interleukin-2; IL2; fusion protein.	
XX		
OS	Unidentified.	
XX		
PN	WO200230566-A2.	
XX		
PD	14-NOV-2002.	
XX		
PF	03-MAY-2002; 2002WO-US013844.	
XX		
PR	03-MAY-2001; 2001US-0288564P.	
XX		
PA	(LEXI-) LEXIGEN PHARM CORP.	
PI	Gillies SD, Lo K, Qian X;	
XX		
DR	WPI; 2003-111985/10.	
DR	N-PSDB; AAD51139.	
XX		
PT	New recombinant anti-EpCAM antibody having an amino acid sequence	
PT	defining an immunoglobulin light or heavy chain framework region, useful	
PT	for the diagnosis, prognosis and treatment of cancer.	
XX		
PS	Disclosure; Page 80-82; 82pp; English.	
XX		
CC	The present invention relates to novel recombinant anti-EpCAM (human	
CC	epithelial cell adhesion molecule) antibodies comprising an amino acid	
CC	sequence defining an immunoglobulin light or heavy chain framework	
CC	region. Sequences of the present invention are useful for the diagnosis,	
CC	prognosis and treatment of cancer. They are also used in gene therapy.	
CC	The present sequence is KS antibody heavy chain-interleukin 2 (IL-2)	
CC	fusion protein. This sequence is used to illustrate the method of the	
CC	invention	
XX		
SQ	Sequence 579 AA;	
XX		
Query Match	89.4%; Score 2744.5; DB 6; Length 579;	
Best Local Similarity	88.5%; Pred. No. 2.1e-132;	
Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;		
QY	1 EVTLVESGQDFVKKPGSLKVSCAASGFAFSHYAMSWRQTPAKRLIEWAVYISGGSGTTY 60	
DB	1 QIQVVGSGAEVKKKRGETVKISCKASGYTFITNGMNVKQIPGKGLKMMGMINTYTGEPY 60	
QY	61 SDSVKGRFTTISRDNAKNTLYIQKRSLSSEDSAMTFCTR-VKLGTYYDSWGCGTTLYSS 119	
DB	61 ADDPKGFAFSLERSTSTAFQIINNLSSEDTATYFCRFRTISKGPY----WGQGSVTYSS 116	
QY	120 ASTGSPVFLPAPSSKSTSGGTALGCLVNDYPEPPTVSGNSGALTSGVHTPAAVYQSS 179	
DB	117 ASTGSPVFLPAPSSKSTSGGTALGCLVNDYPEPPTVSGNSGALTSGVHTPAAVYQSS 176	
QY	180 GLVSLSSVTVVPSSSLGTQTYICNVNKKPSTKVDKVKVEPKSCDKTHTCPCPAPPELLGG 239	
DB	177 GLVSLSSVTVVPSSSLGTQTYICNVNKKPSTKVDKVKVEPKSCDKTHTCPCPAPPELLGG 236	
QY	240 PSVFLPFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAATKPREREQYN 299	
DB	237 PSVFLPFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAATKPREREQYN 296	
QY	300 STYVSVVLTLYLHODMNLGKEVYCKKSNKALPAIEKTIKAGQPREPOVYTLPRERDE 359	
DB	297 STYVSVVLTLYLHODMNLGKEVYCKKSNKALPAIEKTIKAGQPREPOVYTLPRERDE 356	

Oy	360	ITJKNVSLTCLVKGVPSPDI	IAEWBENBNGCPENNKKTP	PVLBDSGFPFLYSKLTVDKSR	419
		ITJKNVSLTCLVKGVPSPDI	IAEWBENBNGCPENNKKTP	PVLBDSGFPFLYSKLTVDKSR	419
Db	357	MTKKNVSLTCLVKGVPSPDI	IAEWBENBNGCPENNKKTP	PVLBDSGFPFLYSKLTVDKSR	416
Oy	420	OOGNVFSCSVMEHALNHNTOKSL	SPGKAPTSSSTKKTOL	BEHLDDLOMTLNGINN	479
		OOGNVFSCSVMEHALNHNTOKSL	SPGKAPTSSSTKKTOL	BEHLDDLOMTLNGINN	479
Db	417	OOGNVFSCSVMEHALNHNTOKSL	SPGKAPTSSSTKKTOL	BEHLDDLOMTLNGINN	476
Oy	480	YKNPXLTRMLTPEKFPYMPKKATEL	KHLQCLUEEBELKPL	EEVYLANAOSXNPHLRPDLISNN	539
		YKNPXLTRMLTPEKFPYMPKKATEL	KHLQCLUEEBELKPL	EEVYLANAOSXNPHLRPDLISNN	539
Db	477	YKNPXLTRMLTPEKFPYMPKKATEL	KHLQCLUEEBELKPL	EEVYLANAOSXNPHLRPDLISNN	536
Oy	540	VIVLELKSGSETTFMGCBYADELTAT	IVYEFNLKRWITFCOSIT	ISTLT	562
		VIVLELKSGSETTFMGCBYADELTAT	IVYEFNLKRWITFCOSIT	ISTLT	562
Db	537	VIVLELKSGSETTFMGCBYADELTAT	IVYEFNLKRWITFCOSIT	ISTLT	579

RESULT 5
 AAO30910
 ID AAO30910 standard; protein; 579 AA.
 XX
 AC AAO30910;
 XX
 DT 22-SEP-2003 (first entry)
 XX
 DE di-KS-ala-IL2 (D20T) variant protein.
 XX
 KM Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
 KM gene therapy; immunoglobulin; Ig; fusion protein; human.
 OS Homo sapiens.
 OS Unidentified.
 OS Chimeric.
 XX
 PN WO2003048334-A2.
 XX
 PD 12-JUN-2003.
 XX
 PE 04-DEC-2002; 2002MO-US038780.
 XX
 PR 04-DEC-2001; 2001US-037113P.
 PR 12-APR-2002; 2002US-0371966P.
 XX
 PA (EMDL-) EMD LEXIGEN RES CENT CORP.
 XX
 PI Gillies SD;
 PI
 DR WPI; 2003-513757/48.
 XX
 PT New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
 PT moiety, useful for preparing a composition for treating cancer, viral
 PT infections or immune disorders.
 XX
 PS Example 10; Page 60-63; 71pp; English.
 XX
 CC The invention relates to cytokine fusion proteins with increased
 CC therapeutic index and methods for increasing the therapeutic index of
 CC such fusion proteins. The fusion protein comprises a non-interleukin-2
 CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
 CC composition for treating cancer, viral infections or immune disorders.
 CC The fusion protein is also used in gene therapy. The present sequence is
 CC di-KS-ala-IL2 (D20T) variant protein comprising di-KS heavy chain fused
 CC to human IL-2 (D20T) variant protein. This sequence is used to illustrate
 CC the method of the invention
 XX
 SQ Sequence 579 AA;
 XX

Query Match	89.2%	Score 2738.5	DB 6	Length 579
Best Local Similarity	88.3%	Pred. No. 4.2e-132		
Matches 515	Conservative 30	Mismatches 373	Indels 5	Gaps 2

Ox 1 EVTLVSGDGFVKPGGSLKVCASGAFPSHIYAMKMWVQTPAKRIELWVAIYSSGGSGTYY 60

Dd	I	QIOLVNSGPELKKRSGSVKISCKACGYYFTTYGNMWMWQAQGLKXMKMGWINTYTGSPTY	60
Qy	61	SDSVKGRFTIISRDNAKNTLYIQMRSILRSDSAMFCTP - VHLGYFYEDSWGQFTTLTVSS	119
Dd	61	ADDFKGRFTIATSTSLTYLQJNNLRSEDATYTCVAFISKDGY ---WQGGTYTVSS	116
Qy	120	ASTKGSVPVPLAPSSKSTSGCTAALGCLVKQYFPPRPTYSVNSGALTSQCHTFPAAVLQSS	179
Dd	117	ASTKGSVPVPLAPSSKSTSGCTAALGCLVKQYFPPRPTYSVNSGALTSQCHTFPAAVLQSS	176
Qy	180	GLVSLSSVTVPPSSISGQTYICANNHPSNTKVDKATPKSPCDKTHTCPPCPAPPELLGG	239
Dd	177	GLVSLSSVTVPPSSISGQTYICANNHPSNTKVDKATPKSPCDKTHTCPPCPAPPELLGG	236
Qy	240	PSYFLPEPKPKOTLMSRTEVTCVVVDVSHEDPEVKENMYVDGVEYHNAATKTRBREQYN	299
Dd	237	PSYFLPEPKPKOTLMSRTEVTCVVVDVSHEDPEVKENMYVDGVEYHNAATKTRBREQYN	296
Qy	300	STTRVAVSVLTVLHQMNLNGEKYKCVSNKALPAPLEKTIISAKAQPREPOVYTLPPSRDE	358
Dd	297	STTRVAVSVLTVLHQMNLNGEKYKCVSNKALPAPLEKTIISAKAQPREPOVYTLPPSRDE	356
Qy	360	LTKQVSLTCLVKGFPSPDIAVEMWSNQPENNYKTPPVLDSQSPFLVSKLTVDSRW	419
Dd	357	MTKQVSLTCLVKGFPSPDIAVEMWSNQPENNYKTPPVLDSQSPFLVSKLTVDSRW	416
Qy	420	QQGNVSCSMHEALNNHYTQKSLSPGKAPTSSSTKKTOLQJLHLLDLQMLNGINN	479
Dd	417	QQGNVSCSMHEALNNHYTQKSAATPAAPTSSTKKTOLQJLHLLDLQMLNGINN	476
Qy	480	YKPKLTRMLTFKFPVPPKATLKHQCLLEELKPLBEVLNLAQSKNPHLRPRDLISNIN	539
Dd	477	YKPKLTRMLTFKFPVPPKATLKHQCLLEELKPLBEVLNLAQSKNPHLRPRDLISNIN	536
Qy	540	VIVLELKSSETTMCCEYADETATVEFLNRMWTFQSIISLTLT	582
Dd	537	VIVLELKSSETTMCCEYADETATVEFLNRMWTFQSIISLTLT	579

RESULT 6
AAB81972
ID AAB81972 standard; protein; 581 AA.
AC AAB81972;
XX
DT 03-JUL-2001 (first entry)
XX
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.
XX
KW Ganglioside; GD2; complementation determining region; CDR; antibody;
KW mouse; cancer.
XX
OS Synthetic.
OS
PN WO200123573-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-JP006773.
XX
PR 30-SEP-1999; 99JP-00278290.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Hanai N, Shitara K, Nakamura K, Niwa R;
XX
DR WPI; 2001-266163/27.
XX
PT Human type complementation-determining domain transplanted antibody and
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of
PT e.g. tumors, has low antigenicity, little side effects but potent
PT activity in cancer.
XX

PS Example 3; Page 111-114; 123pp; Japanese.

XX The present invention describes an antibody, which can react specifically
CC with ganglioside GD2, and is transplanted with a human type
CC complementation-determining domain (CDR), or its fragments. The antibody
CC and its derivatives are useful in diagnosis and therapy of tumors,
CC particularly cancer diagnosis. The present sequence is a protein used in
CC the exemplification of the invention

XX Sequence 581 AA;

Query Match 88.9%; Score 2731.5; DB 4; Length 581;

Best Local Similarity 89.0%; Pred. No. 9,76-132;

Matches 518; Conservative 24; Mismatches 39; Indels 1; Gaps 1;

QY 1 EYLVESGDFVFKGSLKVCASGAFSHYAMSWRQTPAKRLEWAVYISSGSGSTYY 60
DB 1 QVQLQESGPGLVPSQTLSTCTVSGFSLASYNIMHWROPGKLEWLVGMAGGS-TNY 59

QY 61 SDSVKGFTISRDAKNTLYLQMRSLRSDSAMYFCRYVLTGYTPDSMGQGTLLTVSSA 120
DB 60 NSALMSRLTISKDSSKQVFLKMSSTLPAUTAVTYCKAKSDDYSWFAYWGQGLTVSSA 119

QY 121 STKGPSVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSSG 180
DB 120 STKGPSVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSSG 179

QY 181 LYSLSVYVTPSSSLGTQTYICNVNHPKSTKVDKCKEYPCDKHTTCCPPAPBELIGCP 240
DB 180 LYSLSVYVTPSSSLGTQTYICNVNHPKSTKVDKCKEYPCDKHTTCCPPAPBELIGCP 239

QY 241 SVFLPPPKPDITMISRTPEVTCVVDVSHEDPEVKFNMTVDGVEVNAKTKREBOYNS 300
DB 240 SVFLPPPKPDITMISRTPEVTCVVDVSHEDPEVKFNMTVDGVEVNAKTKREBOYNS 299

QY 301 TYRVSIVLTVDHMDNGEKYKCKVSNKALPAIEKTISSAKGQPREPQVYTLPPSRDEL 360
DB 300 TYRVSIVLTVDHMDNGEKYKCKVSNKALPAIEKTISSAKGQPREPQVYTLPPSRDEL 359

QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 420
DB 360 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 419

QY 421 QGNVFSCSVHMEALHNHYTQKSLSLSPGKAPTSSSTKTKLOLEHLILDLOMILNGINNY 480
DB 420 QGNVFSCSVHMEALHNHYTQKSLSLSPGKAPTSSSTKTKLOLEHLILDLOMILNGINNY 479

QY 481 KNPKLTRMLTFKRYMPKATELKHLOCLEBELKPLEEVNLAAOSKNFHLRPDLISINIV 540
DB 480 KNPKLTRMLTFKRYMPKATELKHLOCLEBELKPLEEVNLAAOSKNFHLRPDLISINIV 539

QY 541 IYVELKGSFTTFMCEYADETATIVETFLNRMITFCQSIISTLT 582
DB 540 IYVELKGSFTTFMCEYADETATIVETFLNRMITFCQSIISTLT 581

RESULT 7
ID ADP42961 standard; protein; 575 AA.

XX ADP42961,
XX
XX 23-SEP-2004 (first entry)

XX Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
XX
XX

XX Immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy;
XX cancer; cell surface glycosphingolipid, IL-2.
XX
XX Synthetic.

XX WO2004055056-A1.
XX
XX

PD 01-JUL-2004.

XX 16-DEC-2003; 2003WO-EP014295.

XX 17-DEC-2002; 2002US-0433945P.

XX (MERE) MERCK PATENT GMBH.

XX Gallies SD, Lo K;

XX WPI, 2004-488049/46.

XX N-PSDB; ADP42959.

PT New modified m4.18 antibodies with reduced immunogenicity and that
PT specifically bind the human cell surface glycosphingolipid GD2, useful
PT for treating cancer.

PS Disclosure; SEQ ID NO 6; 51pp; English.

CC The invention relates to a novel antibody variable region, where the
CC antibody variable region specifically binds to human cell surface
CC glycosphingolipid GD2. An antibody variable region of the invention has
CC cytostatic activity, and may have a use in gene therapy. The antibody may
CC be used for treating cancer. The nucleic acid or cell is useful for
CC manufacturing a medicament that may be used for treating diseases such as
CC cancer. The present sequence represents an immunoglobulin heavy chain-IL-
CC 2 fusion protein.

XX Sequence 575 AA;

Query Match 88.4%; Score 2715.5; DB 8; Length 575;

Best Local Similarity 88.8%; Pred. No. 6,36-131;

Matches 517; Conservative 24; Mismatches 34; Indels 7; Gaps 3;

QY 1 EYLVESGDFVFKGSLKVCASGAFSHYAMSWRQTPAKRLEWAVYISSGSGSTYY 60
DB 1 EYLVESGDFVFKGSLKVCASGAFSHYAMSWRQTPAKRLEWAVYISSGSGSTYY 60

QY 61 SDSVKGFTISRDAKNTLYLQMRSLRSDSAMYFCRYVLTGYTPDSMGQGTLLTVSSA 120
DB 61 SDSVKGFTISRDAKNTLYLQMRSLRSDSAMYFCRYVLTGYTPDSMGQGTLLTVSSA 114

QY 121 STKGPSVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSSG 180
DB 121 STKGPSVFLPAPSSKSTSGGTALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSSG 174

QY 181 LYSLSVYVTPSSSLGTQTYICNVNHPKSTKVDKCKEYPCDKHTTCCPPAPBELIGCP 240
DB 181 LYSLSVYVTPSSSLGTQTYICNVNHPKSTKVDKCKEYPCDKHTTCCPPAPBELIGCP 234

QY 241 SVFLPPPKPDITMISRTPEVTCVVDVSHEDPEVKFNMTVDGVEVNAKTKREBOYNS 300
DB 241 SVFLPPPKPDITMISRTPEVTCVVDVSHEDPEVKFNMTVDGVEVNAKTKREBOYNS 294

QY 301 TYRVSIVLTVDHMDNGEKYKCKVSNKALPAIEKTISSAKGQPREPQVYTLPPSRDEL 360
DB 301 TYRVSIVLTVDHMDNGEKYKCKVSNKALPAIEKTISSAKGQPREPQVYTLPPSRDEL 354

QY 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 420
DB 361 TKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRM 414

QY 421 QGNVFSCSVHMEALHNHYTQKSLSLSPGKAPTSSSTKTKLOLEHLILDLOMILNGINNY 480
DB 421 QGNVFSCSVHMEALHNHYTQKSLSLSPGKAPTSSSTKTKLOLEHLILDLOMILNGINNY 473

QY 481 KNPKLTRMLTFKRYMPKATELKHLOCLEBELKPLEEVNLAAOSKNFHLRPDLISINIV 540
DB 481 KNPKLTRMLTFKRYMPKATELKHLOCLEBELKPLEEVNLAAOSKNFHLRPDLISINIV 533

QY 541 IYVELKGSFTTFMCEYADETATIVETFLNRMITFCQSIISTLT 582
DB 541 IYVELKGSFTTFMCEYADETATIVETFLNRMITFCQSIISTLT 575


```
RESULT 8
AA030915
ID  AA030915 standard; protein; 580 AA.
AC  AA030915;
DT  22-SEP-2003 (first entry)
DE  di-NHS76 (gamma4h) (FN>AO) -ala-IL2 (D20T) variant protein.
XX  Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
XX  gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
OS  Homo sapiens.
OS  Unidentified.
OS  Chimeric.
XX  WO2003048334-A2.
XX  PN
XX  PD
XX  12-JUN-2003.
XX  PF  04-DEC-2002; 2002WO-US038780.
XX  PR  04-DEC-2001; 2001US-0337113P.
XX  PR  12-APR-2002; 2002US-0371966P.
XX  PA  (EMDL-) EMD LEXIGEN RES CENT CORP.
XX  PI  Gillies SD;
XX  DR  WPI; 2003-513757/48.
XX  PT  New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX  PT  moiety, useful for preparing a composition for treating cancer, viral
XX  PT  infections or immune disorders.
XX  PS  Example 10; Page 68-71; 71pp; English.
XX  CC  The invention relates to cytokine fusion proteins with increased
XX  CC  therapeutic index and methods for increasing the therapeutic index of
XX  CC  such fusion proteins. The fusion protein comprises a non-interleukin-2
XX  CC  (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX  CC  composition for treating cancer, viral infections or immune disorders.
XX  CC  The fusion protein is also used in gene therapy. The present sequence is
XX  CC  di-NHS76 (gamma4h) (FN>AO) -ala-IL2 (D20T) variant protein comprising di-
XX  CC  KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
XX  CC  is used to illustrate the method of the invention
XX  SQ  Sequence 580 AA;

Query Match      84.4%; Score 2592; DB 6; Length 580;
Best Local Similarity 84.7%; Pred. No. 1.3e-124;
Matches 494; Conservative 31; Mismatches 54; Indels 4; Gaps 3;
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DB 228 PSVFLFPKPKDITLMSRTPEVTCVVVDVSDPEQDFWVVDGVEVHNAKTKPREEQAO 297
QY 300 STYRVSVLTVTHQOMLNQKEVKCKVSKNKAAPATIEKTIISAKGQPREPOVYTLPPSRDE 359
DB 298 STYRVSVLTVTHQOMLNQKEVKCKVSKNKAAPATIEKTIISAKGQPREPOVYTLPPSRDE 357
QY 360 LITKQSVSLCLVKGFPYPSDIAVEMESNQPENNYKTPTPVLDSDGSPFLYSKLTVDKSRW 419
DB 358 MTKQVSLTCLVKGFPYPSDIAVEMESNQPENNYKTPTPVLDSDGSPFLYSKLTVDKSRW 417
QY 420 QGQNVFSCSVHMEALHNHTYTKSLSPGKAPTSSTTKTQQLQHLHLDLMIINGINN 479
DB 418 QGQNVFSCSVHMEALHNHTYTKSATATPGAAPTSSSTTKTQQLQHLHLDLMIINGINN 477
QY 480 YKNPKLTMLTFKFPYPKATLKLQCLEELKPLEEVLNLAOSKNFHLRPRDLISNTN 539
DB 478 YKNPKLTMLTFKFPYPKATLKLQCLEELKPLEEVLNLAOSKNFHLRPRDLISNTN 537
QY 540 VIVLELKSGSETTFMCEVADETATIVEFLNRWITFCOSIISTLT 582
DB 538 VIVLELKSGSETTFMCEVADETATIVEFLNRWITFCOSIISTLT 580

RESULT 9
AA030913
ID  AA030913 standard; protein; 580 AA.
XX  AC  AA030913;
XX  DT  22-SEP-2003 (first entry)
XX  DE  di-NHS76 (gamma2h) (FN>AO) -ala-IL2 (D20T) variant protein.
XX  KM  Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
XX  KM  gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX  OS  Homo sapiens.
XX  OS  Unidentified.
XX  OS  Chimeric.
XX  PN  WO2003048334-A2.
XX  PD  12-JUN-2003.
XX  PF  04-DEC-2002; 2002WO-US038780.
XX  PR  04-DEC-2001; 2001US-0337113P.
XX  PR  12-APR-2002; 2002US-0371966P.
XX  PA  (EMDL-) EMD LEXIGEN RES CENT CORP.
XX  PI  Gillies SD;
XX  DR  WPI; 2003-513757/48.
XX  PT  New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
XX  PT  moiety, useful for preparing a composition for treating cancer, viral
XX  PT  infections or immune disorders.
XX  PS  Claim 37; Page 64-67; 71pp; English.
XX  CC  The invention relates to cytokine fusion proteins with increased
XX  CC  therapeutic index and methods for increasing the therapeutic index of
XX  CC  such fusion proteins. The fusion protein comprises a non-interleukin-2
XX  CC  (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
XX  CC  composition for treating cancer, viral infections or immune disorders.
XX  CC  The fusion protein is also used in gene therapy. The present sequence is
XX  CC  di-NHS76 (gamma2h) (FN>AO) -ala-IL2 (D20T) variant protein comprising di-
XX  CC  KS heavy chain fused to human IL-2 (D20T) variant protein. This sequence
XX  CC  is used to illustrate the method of the invention
XX  SQ  Sequence 580 AA;
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	Query Match Similarity	84.1%	Score 2560;	DB 6;	Length 580;	
	Best Local Similarity	84.1%	Pred No.5,6e-123;			
	Matches	491;	Conservative	31;	Mismatches	36; Indels 6; Gaps 5
Oy	1	EVLTVESGQDFFVKPGSGSLKVSCLASGFAPSH-YAMSWYQTTPAKLEWAVYISSGGSGTY	59			
Dd	1	QVQLQESGPGLVKPSETISLTCAVSGYSISSGYWGMLRPPKGLEWIGSIYHSGS-TY	59			
Oy	60	YSDSKAGFTISRDAKATLYIQMNSLASSEDSAMFCIRVYLGTITYFPSSGCGTTLTVSS	119			
Dd	60	YNPSLKSQSVITISVDISKQFSLKLSSVAADPAVVYCARGKMSK--FYWGCGTLIVTVSS	117			
Oy	120	-ASTGSPVFPLAPASSKSTSGGTALGCLVXDYPPEPTVSNNSGALTSGVTPPAVLQS	178			
Dd	118	CASITGSPVFPLAPASSRSSTSESTAALLGCLVXDYPPEPTVSNNSGALTSGVTHPPAVLS	177			
Oy	179	SGLYSLSASVTVPSSSLGTQTYICNVNHNKPSTKYDKKVEPKSCDKHTHCPCPAPELLG	238			
Dd	178	SGLYSLSASVTVPSSNFQGTQTYTCNVDHKPSNTKYDKXIVEPKSCDKHTHCPCCAP-P-VA	236			
Oy	239	GPSVFLFPKKRKDTLMISRTPEVTVGVVDVSHEDDEVKFNNTVDGVEYVNAKTKREBOY	298			
Dd	237	GPSVFLFPKKRPDITLMISRTPEVTVGVVDVSHEDDEVQFMNVVDGEVNAKTKREBOA	296			
Oy	299	NSTRVNVVLTVLHODMLNGKEYCKCVSNKALPAIEKTISKAKGQPREPOVYTLPPSRD	358			
Dd	297	OSTRVNVSVLVVHODMLNGKEYCKCVSNKGLPAIEKTIISTKKGQPREPOVYTLPPSRD	356			
Oy	359	ELTNQVSLTCLVKGFIYPSDIADVEMESNGQPENNRYKTPPVLDSDGSFFLYSKLTVDSKR	418			
Dd	357	EMTKNQVSLTCLVKGFIYPSDIADVEMESNGQPENNYKTPPMULDSDGSFFLYSKLTVDSKR	416			
Oy	419	WQQGVFSCSYMHETLNHYTKQSLSTSPGARPTSSSTRTKTKQLOLEHLILLDLQMTLNGIN	478			
Dd	417	WQQGVFSCSYMHETLNHYTKQSAVTATPGAAPTSSSTRTKTKQLOLEHLILLDLQMTLNGIN	476			
Oy	479	NYKNPKLTRMLTFPKFMPKKAATELKGLCCEBELKPLEEVLNLIAOSKNFHLPRLDISNI	538			
Dd	477	NYKNPKLTRMLTFPKFMPKKAATELKGLCCEBELKPLEEVLNLIAOSKNFHLPRLDISNI	536			
Oy	539	NVIVLELKGSETTFMCYEADETTATIVBEFLNRNITFCQGISITLT	582			
Dd	537	NVIVLELKGSETTFMCYEADETTATIVBEFLNRNITFCQGISITLT	580			
	RESULT 10					
	AAO18400					
	ID AAO18400 standard; protein; 449 AA.					
AC	AAO18400;					
XX						
XX	11-OCT-2002 (first entry)					
XX						
DE	Mature humanised murine CBE11 heavy chain variable domain.					
KV	Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;					
KW	neoplasm; Lr-beta-R; light chain; heavy chain; variable region.					
XX						
OS	Mus sp.					
OS	Synthetic.					
PN	WC0200230986-A2.					
XX						
PD	18-APR-2002.					
XX						
XX	12-OCT-2001, 2001WO-US032140.					
PF						
PR	13-OCT-2000; 2000US-0240285P.					
PR	13-MAR-2001; 2001US-0275289P.					
RR	21-JUN-2001; 2001US-0299987P.					
XX						
PA	(BIOJ) BIOGEN INC.					

[illegible]

```
XX 03-OCT-2003; 2003WO-US031420.
XX PF
XX KW
XX PR 03-OCT-2002; 2002US-0415940P.
XX (LARG-) LARGE SCALE BIOLOGY CORP.
XX PA
XX PI Reini SJ, Edwards P;
XX DR WPI; 2004-330170/30.
XX DR N-PSDB; ADN97489.
XX PT New artificial proprotein comprises three peptide sequences, useful for
XX PT artificial multimeric protein engineering in eukaryotes.
XX PS Example 15; SEQ ID NO 64; 244pp; English.
XX CC The invention relates to an artificial proprotein comprising three
XX CC peptide sequences: a first peptide sequence of interest, a propeptide
XX CC sequence attached to the C-terminus of the first peptide sequence of
XX CC interest, and a second peptide of interest attached to the C-terminus of
XX CC the propeptide sequence. The artificial proprotein and polynucleotides
XX CC are useful for artificial multimeric protein engineering, e.g. antibodies
XX CC and antibody fragments in eukaryotes. This sequence corresponds to a
XX CC protein used in the generation of the protein of the invention.
XX SQ Sequence 713 AA;
XX
XX Query Match 72.2%; Score 2216; DB 8; Length 713;
XX Best Local Similarity 91.7%; Pred. No. 2.6e-105;
XX Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;
QY 1 EYTLVSGGDFYKPGGSLKVCAGAFAPSHYAMSWVROTAPKRLBFWAYISSGSGSTYY 60
DB 257 EYDLVSGGDLVKGPGSLKVCAGAFAPSHYAMSWVROTAPKRLBFWAYISSGSGSTYY 316
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYCTRYKL-----GTYFF--DSWGOG 112
DB 317 PDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYCTRYKL-----GTYFF--DSWGOG 376
QY 113 TTLTVSSASTKGPVSFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNMSGALTSQVHTF 172
DB 377 ASVTYSASTKGPVSFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNMSGALTSQVHTF 436
QY 173 PAVLOSGLYSLSVYTVVSSSLGTQTYICNVNHRKPSNTKVDKQVEPKSCDTHTCPCPC 232
DB 437 PAVLOSGLYSLSVYTVVSSSLGTQTYICNVNHRKPSNTKVDKQVEPKSCDTHTCPCPC 496
QY 233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKT 292
DB 497 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKT 556
QY 293 PREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 352
DB 557 PREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 616
QY 353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 412
DB 617 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 676
QY 413 TVDKSRMOQGNVFSQSVMEHALHNHYTOKSLSLSPCK 449
DB 677 TVDKSRMOQGNVFSQSVMEHALHNHYTOKSLSLSPCK 713
RESULT 12
ADN97489
ID ADN97489 standard; protein; 715 AA.
XX
XX AC ADN97489;
XX
XX 01-UTL-2004 (first entry)
XX
```

```
DE Artificial protein construction protein #3.
XX
XX KW artificial proprotein; propeptide; protein engineering; antibody.
XX OS Unidentified.
XX PN WO2004031362-A2.
XX PD 15-APR-2004.
XX PF 03-OCT-2003; 2003WO-US031420.
XX XX
XX PR 03-OCT-2002; 2002US-0415940P.
XX PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX PI Reini SJ, Edwards P;
XX DR WPI; 2004-330170/30.
XX DR N-PSDB; ADN97488.
XX PT New artificial proprotein comprises three peptide sequences, useful for
XX PT artificial multimeric protein engineering in eukaryotes.
XX PS Example 15; SEQ ID NO 62; 244pp; English.
XX CC The invention relates to an artificial proprotein comprising three
XX CC peptide sequences: a first peptide sequence of interest, a propeptide
XX CC sequence attached to the C-terminus of the first peptide sequence of
XX CC interest, and a second peptide of interest attached to the C-terminus of
XX CC the propeptide sequence. The artificial proprotein and polynucleotides
XX CC are useful for artificial multimeric protein engineering, e.g. antibodies
XX CC and antibody fragments in eukaryotes. This sequence corresponds to a
XX CC protein used in the generation of the protein of the invention.
XX SQ Sequence 715 AA;
XX
XX Query Match 72.2%; Score 2216; DB 8; Length 715;
XX Best Local Similarity 91.7%; Pred. No. 2.6e-105;
XX Matches 419; Conservative 10; Mismatches 20; Indels 8; Gaps 2;
QY 1 EYTLVSGGDFYKPGGSLKVCAGAFAPSHYAMSWVROTAPKRLBFWAYISSGSGSTYY 60
DB 259 EYDLVSGGDLVKGPGSLKVCAGAFAPSHYAMSWVROTAPKRLBFWAYISSGSGSTYY 318
QY 61 SDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYCTRYKL-----GTYFF--DSWGOG 112
DB 319 PDSVKGRTISRDNKNTLYLQMRSLRSEDSAMYCTRYKL-----GTYFF--DSWGOG 378
QY 113 TTLTVSSASTKGPVSFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNMSGALTSQVHTF 172
DB 379 ASVTYSASTKGPVSFPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNMSGALTSQVHTF 438
QY 173 PAVLOSGLYSLSVYTVVSSSLGTQTYICNVNHRKPSNTKVDKQVEPKSCDTHTCPCPC 232
DB 439 PAVLOSGLYSLSVYTVVSSSLGTQTYICNVNHRKPSNTKVDKQVEPKSCDTHTCPCPC 498
QY 233 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKT 292
DB 499 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYDGEVHNAAKT 558
QY 293 PREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 352
DB 559 PREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVY 618
QY 353 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 412
DB 619 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 678
QY 413 TVDKSRMOQGNVFSQSVMEHALHNHYTOKSLSLSPCK 449
DB 679 TVDKSRMOQGNVFSQSVMEHALHNHYTOKSLSLSPCK 715
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RESULT 13
ADM47075
ID ADM47075 standard; protein; 475 AA.
XX
XX ADM47075;
XX
XX 03-JUN-2004 (first entry)
XX
XX Mouse anti-human G-CSF antibody heavy chain protein.
XX
XX methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;
XX 6-mannosyl transferase; alpha-1; 2-mannosidase;
XX orotidin-5'-phosphate decarboxylase; UBA3;
XX phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADL1;
XX imidazole-glycerol-phosphate dehydratase; HIS3;
XX 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;
XX PEP4; YPS1; KTR1; MNN9; AOX; GAPDH; mannosyl transferase;
XX glyceraldehyde 3-phosphate dehydrogenase; mannosyl glycoprotein.
XX
XX Mus sp.
XX
XX WO2003091431-A1.
XX
XX 06-NOV-2003.
XX
XX 28-APR-2003; 2003WO-JP005464.
XX
XX 26-APR-2002; 2002JP-00127677.
XX
XX (KIRI ) KIRIN BEER KK.
XX (NABD ) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX Kobayashi K, Kitagawa Y, Komeda T, Kawashima N, Jigami Y,
XX Chiba Y;
XX
XX WPI; 2003-854401/79.
XX
XX Producing methylotroph yeast that expresses mammalian sugar chains by
XX disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
XX
XX Example 28; SEQ ID NO 94; 247bp; Japanese.
XX
XX The invention relates to the production of a methylotroph yeast that
XX produces mammalian sugar chains, comprising disrupting the OCH1 gene in
XX the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
XX and expressing the alpha-1,2-mannosidase gene. The specification also
XX includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
XX (UBA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
XX (ADL1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
XX isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
XX (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
XX aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol
XX oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
XX sequences. The yeast is used for the production of human and mammalian
XX high mannose glycoproteins with high yield and purity. The method is also
XX useful for producing hybrid or complex sugar chains containing mammalian
XX type chains. This sequence represents a mouse anti-human G-CSF antibody
XX heavy chain used in the invention.
XX
XX Sequence 475 AA:
XX
XX Query Match 71.9%; Score 2209.5; DB 7; Length 475;
XX Best Local Similarity 91.2%; Pred. No. 3.7e-105;
XX Matches 416; Conservative 15; Mismatches 18; Indels 7; Gaps 2;
XX
XX 1 EYLVSSGDFVKGSLKSCAAGFAFSHYAMSWRQPARLEAVAYISGGSGTYY 60
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX 20 EYLVSSGDFVKGSLKSCAAGFAFSHYAMSWRQPARLEAVAYISGGSGTYY 79
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 61 SDVSKRFTISRDNANKTLYLQNRSLRSEDSAMFYCTRVLT-----GTYV---DSWQGT 113
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX 80 ADSVKRFTISRDNANKTLYLQNRSLRSEDSAMFYCTRVLT-----GTYV---DSWQGT 139

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XX QY 114 TLTVSSASTKGPSPPLAPSSKSTSGTALAGLVNDYFPEPTVSMNSGALTSGVHTP 173
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 140 TVTVSSASTKGPSPPLAPSSKSTSGTALAGLVNDYFPEPTVSMNSGALTSGVHTP 199
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX QY 174 AVLOSSGLYSLSSTVTPSSSLGTQTYI CVMNHPKSPNTKVKKVPEKSCDKHTTCCPCPA 233
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 200 AVLOSSGLYSLSSTVTPSSSLGTQTYI CVMNHPKSPNTKVKKVPEKSCDKHTTCCPCPA 259
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX QY 234 PELLGSPVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGEVHNAAKTP 293
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 260 PELLGSPVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNKYVDGEVHNAAKTP 319
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX QY 294 REEQVNSTRVSVTLVTHQDMLNGKEYCKVKSNKLPAPIEKTISKAKGQPREPOVYTL 353
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 320 REEQVNSTRVSVTLVTHQDMLNGKEYCKVKSNKLPAPIEKTISKAKGQPREPOVYTL 379
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 413
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT 439
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX QY 414 VDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 449
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX DB 440 VDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 475
XX |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
XX
XX RESULT 14
XX AAR47453
XX ID AAR47453 standard; protein; 477 AA.
XX
XX AAR47453;
XX
XX 25-MAR-2003 (revised)
XX DT 24-JUN-1994 (first entry)
XX
XX chIT84.12 H3 heavy chain.
XX
XX Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region;
XX transform; myeloma cell; light chain; tumour.
XX
XX Synthetic.
XX
XX WO9325237-A1.
XX
XX 23-DEC-1993.
XX
XX 15-JUN-1993; 93WO-US005709.
XX
XX 15-JUN-1992; 92US-00904074.
XX
XX (YANG/) YANG Y.
XX (CITY ) CITY OF HOPE.
XX
XX Shively JB, Fischer R, Wu A, Paxton R, Yang YH;
XX
XX WPI; 1994-007204/01.
XX
XX N-PSDB; AA054655.
XX
XX New chimeric T 84.12 antibody active against carcinoembryonic antigen -
XX has murine variable and human constant regions, also DNA encoding it and
XX transformed myeloma cells.
XX
XX Claim 1; Page 22-23; 27pp; English.
XX
XX The sequences (AA054651-52) show the light and heavy chain cDNAs of
XX murine T84.12. The T84.12 antibody is directed against the tumour marker
XX carcinoma embryonic antigen, and is useful for tumour imaging and
XX immunotherapy. The amino acid sequence given in the specification has
XX been incorrectly identified as a nucleic acid sequence, therefore
XX unacceptable characters have been represented as an 'N'. The amino acid
XX sequence given below has been derived from the cDNA, by the indexer.
XX (Updated on 25-MAR-2003 to correct PN field.)

```

SQ Sequence 477 AA;

Query Match 71.8%; Score 2205; DB 2; Length 477;

Best Local Similarity 92.5%; Pred. No. 6,3e-105; Matches 419; Conservative 8; Mismatches 18; Indels 8; Gaps 3;

QY 1 EYTLVESGGDFPKPGSLKLVSCAAGFAFASHYAMSWKOTPAKRLIEWVAIISGGSGTYY 60
 DB EYTLVESGGDFPKPGSLKLVSCAAGFAFASHYAMSWKOTPAKRLIEWVAIISGGSGTYY 87

QY 61 SDSVKGPRFTISRDNANKNTLYLQMSLRSDSAMFCTRYKLGTY---FDSMGQGTLLT 116
 DB VDSVKGPRFTISRDNANKNTLYLQMSLRSDSAMFCTRYKLGTY---DYGGGGFGYWGQGTLLT 144

QY 117 VSSASTKGPSVFPPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVL 176
 DB 145 VSAASTKGPSVFPPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVL 204

QY 177 QSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKEPKSCDKTHHTCPCPAPRL 236
 DB 205 QSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKEPKSCDKTHHTCPCPAPRL 264

QY 237 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
 DB 265 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 324

QY 297 QYNSTYRVVSVLTTLHODMLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPS 356
 DB 325 QYNSTYRVVSVLTTLHODMLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPS 384

QY 357 RDELTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 416
 DB 385 RDELTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 444

QY 417 SRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
 DB 445 SRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 477

RESULT 15

ADM72029 standard; protein; 471 AA.

ADM72029;

03-JUN-2004 (first entry)

Chimeric mouse-human antibody M19B11 heavy chain.

GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer; cytostatic; M19B11.

Mus sp.

Homo sapiens.

Chimeric.

WO2004022739-A1.

18-MAR-2004.

04-SEP-2003; 2003WO-JP011318.

04-SEP-2002; 2002WO-JP008999.

(CHUS) CHUGAI SEIYAKU KK.

Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;

MPI; 2004-269573/25.

N-PSDB; ADM72028.

Antibody against the N terminus of glypican 3 (GPC3) causes cell disruption and is useful as an anticancer agent.

XX Example 4; SEQ ID NO 14; 122pp; Japanese.

PS The invention relates to an antibody against the N terminus of glypican 3
 CC (GPC3). The antibody can be used for causing cell disruption and can be
 CC uses as an anti-cancer agent. The present sequence represents a chimeric
 CC mouse-human antibody M19B11 heavy chain.

SQ Sequence 471 AA;

Query Match 71.8%; Score 2203.5; DB 8; Length 471;

Best Local Similarity 92.3%; Pred. No. 7.5e-105; Matches 418; Conservative 9; Mismatches 21; Indels 5; Gaps 2;

QY 1 EYTLVESGGDFPKPGSLKLVSCAAGFAFASHYAMSWKOTPAKRLIEWVAIISGGSGTYY 60
 DB 20 EYTLVESGGDFPKPGSLKLVSCAAGFAFASHYAMSWKOTPAKRLIEWVAIISGGSGTYY 79

QY 61 SDSVKGPRFTISRDNANKNTLYLQMSLRSDSAMFCTRYKLGTY---YFDSMGQGTLLT 116
 DB 80 PPTMDRFTISRDNANKNTLYLQMSLRSDTAFYHCTRHN--GGENYGFAYWGQGTLLT 138

QY 117 VSSASTKGPSVFPPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVL 176
 DB 139 VSAASTKGPSVFPPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHPFPAVL 198

QY 177 QSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKEPKSCDKTHHTCPCPAPRL 236
 DB 199 QSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKEPKSCDKTHHTCPCPAPRL 258

QY 237 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 296
 DB 259 LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 318

QY 297 QYNSTYRVVSVLTTLHODMLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPS 356
 DB 319 QYNSTYRVVSVLTTLHODMLNGKEYCKVSNKALPAPIEKTI SKAKGQPREPOVYTLPPS 378

QY 357 RDELTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 416
 DB 379 RDELTKNOVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 438

QY 417 SRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
 DB 439 SRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 471

Search completed: December 23, 2004, 18:57:43
 Job time : 157.692 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:39 ; Search time 38.4376 Seconds
(Without alignments)
1004.148 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071
Sequence: 1 EVTLVSGGDFVKGSLK.....IVEFLNRMTFCGSIITLT 582

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5A COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6A COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6B COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/PC/US COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2153.5	70.1	459	1 US-08-157-101A-7	Sequence 7, Appl
2	2149.5	70.0	452	3 US-09-027-449-71	Sequence 71, Appl
3	2149.5	70.0	452	3 US-09-026-985-71	Sequence 71, Appl
4	2149.5	70.0	452	4 US-09-121-952A-71	Sequence 71, Appl
5	2149.5	70.0	452	4 US-09-234-340A-71	Sequence 71, Appl
6	2124	69.2	453	3 US-08-466-151-8	Sequence 8, Appl
7	2124	69.2	453	3 US-08-466-163B-8	Sequence 8, Appl
8	2124	69.2	453	4 US-08-802-096-8	Sequence 8, Appl
9	2124	69.2	453	4 US-08-802-077-8	Sequence 8, Appl
10	2122	69.1	451	2 US-08-887-352B-14	Sequence 14, Appl
11	2122	69.1	451	2 US-08-887-352B-16	Sequence 16, Appl
12	2122	69.1	451	3 US-08-466-151-65	Sequence 65, Appl
13	2122	69.1	451	3 US-09-109-207C-14	Sequence 14, Appl
14	2122	69.1	451	3 US-09-109-207C-16	Sequence 16, Appl
15	2122	69.1	451	3 US-09-286-005-14	Sequence 14, Appl
16	2122	69.1	451	3 US-09-286-005-16	Sequence 16, Appl
17	2122	69.1	451	4 US-09-920-171-14	Sequence 14, Appl
18	2122	69.1	451	4 US-09-920-171-16	Sequence 16, Appl
19	2122	69.1	451	4 US-09-716-028-14	Sequence 14, Appl
20	2122	69.1	451	4 US-09-716-028-16	Sequence 16, Appl
21	2122	69.1	451	4 US-10-113-996-16	Sequence 16, Appl
22	2122	69.1	451	2 US-08-867-352B-18	Sequence 18, Appl
23	2118	69.0	451	3 US-09-109-207C-18	Sequence 18, Appl
24	2118	69.0	451	3 US-09-282-505-2	Sequence 2, Appl
25	2118	69.0	451	3 US-09-054-255-18	Sequence 18, Appl
26	2118	69.0	451	3 US-09-296-005-18	Sequence 18, Appl
27	2118	69.0	451	3 US-09-296-005-18	Sequence 18, Appl

28	2118	69.0	451	4 US-09-282-846-2	Sequence 2, Appl
29	2118	69.0	451	4 US-09-680-145-2	Sequence 2, Appl
30	2118	69.0	451	4 US-09-920-171-18	Sequence 18, Appl
31	2118	69.0	451	4 US-09-716-028-18	Sequence 18, Appl
32	2118	69.0	451	4 US-09-483-588-2	Sequence 2, Appl
33	2118	69.0	451	4 US-10-113-996-18	Sequence 18, Appl
34	2115.5	68.9	449	3 US-09-679-397-2	Sequence 2, Appl
35	2115.5	68.9	449	3 US-09-680-148-2	Sequence 2, Appl
36	2115.5	68.9	449	4 US-09-304-465A-2	Sequence 2, Appl
37	2102	68.4	449	1 US-08-458-516-13	Sequence 13, Appl
38	2097	68.3	478	3 US-08-487-550-8	Sequence 8, Appl
39	2097	68.3	478	4 US-09-526-098-8	Sequence 8, Appl
40	2097	68.3	478	4 US-09-383-916-8	Sequence 8, Appl
41	2066	67.3	711	3 US-09-485-737B-90	Sequence 90, Appl
42	2063	67.2	468	3 US-09-485-737B-67	Sequence 67, Appl
43	2052.5	66.8	467	3 US-08-030-175-42	Sequence 42, Appl
44	2052	66.8	476	2 US-08-378-939-10	Sequence 10, Appl
45	2049.5	66.7	467	4 US-08-030-175-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-08-157-101A-7

; Sequence 7, Application US/08157101A

; Patent No. 5808032

; GENERAL INFORMATION:

; APPLICANT: KURIHARA, TATSUYA

; APPLICANT: MATSUKURA, SHIGEKAZU

; APPLICANT: TSURUOKA, NOBUO

; APPLICANT: NISHIHARA, KENJI

; APPLICANT: NISHIHARA, TATSURO

; TITLE OF INVENTION: ANTI-HBc ANTIBODY GENES AND EXPRESSION

; TITLE OF INVENTION: PLASMIDS THEREFOR

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PILLSBURY, MADISON & SUTRO

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08157,101A

; FILING DATE: 05-APR-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: TITUS, MARIANA K

; REGISTRATION NUMBER: 35843

; REFERENCE/DOCKET NUMBER: 9437/204199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3711

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUCH

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 459 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-157-101A-7

Query Match 70.1%; Score 2153.5; DB 1; Length 459;
Best Local Similarity 89.8%; Pred. No. 1.3e-159;
Matches 404; Conservative 20; Mismatches 25; Indels 1;

Qy	1	EVLVBSGGPFVPRGSLKXSCAASFAFSHAMWNRQTPAKRLIEWAIVSSGGSGTTY	60
Db	10	QVQVLBSGGGVVPRGSLRLSCAASFTTSSNSMFWQAPEKGLIEWAVAILYDGNHKFY	69
Qy	61	SDSVKGRFTISRDNANKNTYLQWRSLRSDSAMFCTRVK-LGTYYPDSWGQGTTLTVSS	119
Db	70	ADSVKGRFTISRDNANKNTYLLEKYSLGTEDEDTGVYICIRDQYGVHFRFDSMGQGLTVVSS	129
Qy	120	ASTKGPVFPPLAASSKTSGGTAAAGCYKQVPEPPVTVSNNSGALTSGCYHTPPAVYQSS	179
Db	130	ASTKGPVFPPLAASSKTSGGTAAAGCYKQVPEPPVTVSNNSGALASGVHTPPAVIQSS	189
Qy	180	GLYSLSSVTVPESSSLGTQTYICNVNHNKSNKVDKATPEKSCDXTHTCPCPAPELLGG	239
Db	190	GLYSLSSVTVPESSSLGTQTYICNVNHNKSNKVDKATPEKSCDXTHTCPCPAPELLGG	249
Qy	240	PSVFLPPPKKDTLMTSRTPRYTCVVVDVSHEDPEVKATMYVDGYEVNAAATKPREBOYN	299
Db	250	PSVFLPPPKKDTLMTSRTPRYTCVVVDVSHEDPEVKATMYVDGYEVNAAATKPREBOYN	309
Qy	300	STRVAVSVLTVLHQDLNMGKEKCKKSNALPAPIEKTIISAKGQPREPOVYTLPPSRDE	359
Db	310	STRVAVSVLTVLHQDLNMGKEKCKKSNALPAPIEKTIISAKGQPREPOVYTLPPSRDE	369
Qy	360	LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDYDSRW	419
Db	370	LTRKQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDYDSRW	429
Qy	420	QQGNVFSCTSMHALLNHYTQKSLSPCK	449
Db	430	QQGNVFSCTSMHALLNHYTQKSLSPCK	459

RESULT 2
 US-09-027-449-71
 : Sequence 71, Application US/09027449
 : Patent No. 6023158
 : GENERAL INFORMATION:
 : APPLICANT: Gonzalez, Tania R.
 : APPLICANT: Leong, Steven R.
 : APPLICANT: Presta, Leonard G.
 : TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 : TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 : NUMBER OF SEQUENCES: 72
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/027,449
 : FILING DATE: 20-Feb-1998
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/074,330
 : FILING DATE: 22-Jan-1998
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/038,664
 : FILING DATE: 21-Feb-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Love, Richard B.
 : REGISTRATION NUMBER: 34,659
 : REFERENCE/DOCKET NUMBER: P1085R3-2
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650/225-5530
 : TELEFAX: 650/952-9881

```

: INFORMATION FOR SEQ ID NO: 71:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 452 amino acids
:
: TYPE: Amino Acid
:
: TOPOLOGY: Linear
:
US-09-027-449-71

```

Query Match	70.0%;	Score 2149.5;	DB 3;	Length 452;
Best Local Similarity	88.7%;	Pred. No. 2.6e-159;		
Matches 401; Conservative	19;	Mismatches 29;	Indels 3;	Gaps 1;

QY	1	EVLTVESGGDLPFKPGGSLKLVSCAASGAFPSHYAASWVROTPAKRLVNAVAISSGSGGTY	60
Db	1	EVQVLVSGGGGLVQPGGSLRLSCAASGYSFSSHYHWVRQAPKGQLEWVGVIIDPSNBEITY	60
QY	61	SDSVKGRFTISNDNAKNTLLYLQMSLRSEDSAMFTCTRVKL--GIYYDPMSGGGTTLY	117
Db	61	NOAFKGRFTLSRDNDSKNKNTAYLLQMSLRREDYAVVYGCARGDYRYVNGDAFFPWGGGTLVTV	120
QY	118	SSASTGSPVFPFLAASKSTSGGTALGLVKDVPFPVTVSNMGSALTSGVHTFPVVLQ	177
Db	121	SSASTGSPVFPFLAASKSTSGGTALGLVKDVPFPVTVSNMGSALTSGVHTFPVVLQ	180
QY	178	SSGLYSLSSVVVPSSSLGTQTYICNVNHNKSNKRVDKVPEKSCDTHTCPCPAPELL	237
Db	181	SSGLYSLSSVVVPSSSLGTQTYICNVNHNKSNKRVDKVPEKSCDTHTCPCPAPELL	240
QY	238	GGSPVFLPPPKKQDTLMSRTPREVTVVVVDVSHEDPEVKFMYVDGVYVNAKTKPREEQ	297
Db	241	GGSPVFLPPPKKQDTLMSRTPREVTVVVVDVSHEDPEVKFMYVDGVYVNAKTKPREEQ	300
QY	298	VNSTYRVVSVLVLYHQDMLNGEKYCKSNALPAPIEKTISKAGQPREPOVYTLPPSR	357
Db	301	VNSTYRVVSVLVLYHQDMLNGEKYCKSNALPAPIEKTISKAGQPREPOVYTLPPSR	360
QY	358	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPRENNKTPPEVLDSGSFFLYSKLTIVDKS	417
Db	361	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPRENNKTPPEVLDSGSFFLYSKLTIVDKS	420
QY	418	RMQGGVFPSCSYMHEALNNHTQSLSLSPCK	449
Db	421	RMQGGVFPSCSYMHEALNNHTQSLSLSPCK	452

RESULT 3
 US-09-026-985-71
 Sequence 71, Application US/09026985
 Patent No. 6133426
 GENERAL INFORMATION:
 APPLICANT: Gonzalez, Tania R.
 APPLICANT: Leong, Steven R.
 APPLICANT: Presta, Leonard G.
 TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/026,985
 FILING DATE: 20-Feb-1998
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R3-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-09-026-985-71

Query Match 70.0%; Score 2149.5; DB 3; Length 452;
 Best Local Similarity 88.7%; Pred. No. 2,6e-159;

Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EYLVESGGDFYKPGSLKVCASGAPFSHYAMSVROTAPARLEWVAISSGSGGTY 60
 DB 1 EYLVESGGDFYKPGSLKVCASGAPFSHYAMSVROTAPARLEWVAISSGSGGTY 60
 QY 61 SDSVGRFTISRDNKNTLYLQMSLRSEDSAMVFCRTVKL--GTYFDSWGQGTLLV 117
 DB 61 NQKFKGRFTLSRDNKNTLYLQMSLRSEDSAMVFCRTVKL--GTYFDSWGQGTLLV 120
 QY 118 SASTGSPSVFLAPSPSKTSSTGTAALGCLVQDYFEPPTVSNAGALTSVHTTFAVLD 177
 DB 121 SASTGSPSVFLAPSPSKTSSTGTAALGCLVQDYFEPPTVSNAGALTSVHTTFAVLD 180
 QY 178 SSGLYSLSSVTVVPSSSLGTYIYICNVNHPSTKYDKVPEKSCDKHTCPCPAPPELL 237
 DB 181 SSGLYSLSSVTVVPSSSLGTYIYICNVNHPSTKYDKVPEKSCDKHTCPCPAPPELL 240
 QY 238 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVHNATKPREQ 297
 DB 241 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVHNATKPREQ 300
 QY 298 YNSTRVSVVLTVLHODMNGKEYKCKVSNKALPAPIETKISAKAQPREPQVYTLPPSR 357
 DB 301 YNSTRVSVVLTVLHODMNGKEYKCKVSNKALPAPIETKISAKAQPREPQVYTLPPSR 360
 QY 358 DELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDS 417
 DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDS 420
 QY 418 RMQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 449
 DB 421 RMQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 452

RESULT 4

US-09-121-952A-71
 Sequence 71, Application US/09121952A

GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., Heel, Vanessa

APPLICANT: Kouments, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Shahrokh, Zahra

APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES

TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/121,952A
 FILING DATE: 24-Jul-1998
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/074330
 FILING DATE: 22-JAN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/075467
 FILING DATE: 20-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-09-121-952A-71

Query Match 70.0%; Score 2149.5; DB 4; Length 452;
 Best Local Similarity 88.7%; Pred. No. 2,6e-159;

Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EYLVESGGDFYKPGSLKVCASGAPFSHYAMSVROTAPARLEWVAISSGSGGTY 60
 DB 1 EYLVESGGDFYKPGSLKVCASGAPFSHYAMSVROTAPARLEWVAISSGSGGTY 60
 QY 61 SDSVGRFTISRDNKNTLYLQMSLRSEDSAMVFCRTVKL--GTYFDSWGQGTLLV 117
 DB 61 NQKFKGRFTLSRDNKNTLYLQMSLRSEDSAMVFCRTVKL--GTYFDSWGQGTLLV 120
 QY 118 SASTGSPSVFLAPSPSKTSSTGTAALGCLVQDYFEPPTVSNAGALTSVHTTFAVLD 177
 DB 121 SASTGSPSVFLAPSPSKTSSTGTAALGCLVQDYFEPPTVSNAGALTSVHTTFAVLD 180
 QY 178 SSGLYSLSSVTVVPSSSLGTYIYICNVNHPSTKYDKVPEKSCDKHTCPCPAPPELL 237
 DB 181 SSGLYSLSSVTVVPSSSLGTYIYICNVNHPSTKYDKVPEKSCDKHTCPCPAPPELL 240
 QY 238 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVHNATKPREQ 297
 DB 241 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVHNATKPREQ 300
 QY 298 YNSTRVSVVLTVLHODMNGKEYKCKVSNKALPAPIETKISAKAQPREPQVYTLPPSR 357
 DB 301 YNSTRVSVVLTVLHODMNGKEYKCKVSNKALPAPIETKISAKAQPREPQVYTLPPSR 360
 QY 358 DELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDS 417
 DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDS 420
 QY 418 RMQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 449
 DB 421 RMQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 452

RESULT 5

US-09-234-340A-71
 Sequence 71, Application US/09234340A

GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., Heel, Vanessa

APPLICANT: Kouments, Iphigenia

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-Feb-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-71

Query Match 70.0%; Score 2149.5; DB 4; Length 452;
Best Local Similarity 88.7%; Pred. No. 2.6e-159;
Matches 401; Conservative 19; Mismatches 29; Indels 3; Gaps 1;

QY 1 EVTVLVSQGDVFKPGGSLKVGSCAGAFASHTAMSVROTAPAKRLLEWAVYISSGSGGTY 60
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHVRQAPGKLEWVGVIDPSNGETTY 60
QY 61 SDSVKGRFTISRDNKNTLYLQMRLSRSDSAMVFCRTVKL--GTYFDSWGQGTTLTV 117
DB 61 NQKPKRFTLSRDNSKNTAYLQNSLRADDTAVYICARDYRNGDMFVDVWGQGLTVTV 120
QY 118 SASSTKGPSVFPPLAPSSKSTSGTAAAGCLVNDYPEPEVTWNSGALTSGVHTPPAVLQ 177
DB 121 SASSTKGPEVFPPLAPSSKSTSGTAAAGCLVNDYPEPEVTWNSGALTSGVHTPPAVLQ 180
QY 178 SSGGLYSLSVTVVPSSSLGTOTYICVNHKPSNTKYDKVEPKSCDKTHTCPPAPPELL 237
DB 181 SSGGLYSLSVTVVPSSSLGTOTYICVNHKPSNTKYDKVEPKSCDKTHTCPPAPPELL 240
QY 238 GGPSPVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVFNMYVDSGEVHNAAKTRREQ 297
DB 241 GGPSPVFLPPKPKDMLMISRTPEVTCVVVDVSHEDPEVFNMYVDSGEVHNAAKTRREQ 300
QY 298 YNSTRVVSVLTQLVQDMNLNGEKYKCVSNKALPAPIEKTISKAKQPREPOVYTLPPSR 357
DB 301 YNSTRVVSVLTQLVQDMNLNGEKYKCVSNKALPAPIEKTISKAKQPREPOVYTLPPSR 360
QY 358 DELTKNQVSLTCLVKGFPYSIDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 417
DB 361 EEMTKNQVSLTCLVKGFPYSIDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 420

QY 418 RMOQGNVSCSYMEALNHYTQKSLSPGK 449
DB 421 RMOQGNVSCSYMEALNHYTQKSLSPGK 452

RESULT 6
US-08-466-151-8
Sequence 8, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Pardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-Mar-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-Jan-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-May-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-Aug-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-8

Query Match 69.2%; Score 2124; DB 3; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.6e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;

QY 1 EVTVLVSQGDVFKPGGSLKVGSCAGAFASHTAMSVROTAPAKRLLEWAVYISSGSGGTY 59
DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGYSITSGYSNMWIRQAPGKLEWVASITYGDS-TN 59
QY 60 YDSVYKGRFTISRDNKNTLYLQNSLRSDSAMVFCRTVK--LGTYYFDSWGQGTTLTV 117
DB 60 YDSVYKGRFTISRDNKNTLYLQNSLRADDTAVYICARGSYRFGHMHAAVWGQGLTVTV 119
QY 118 SASST--KGPSVFPPLAPSSKSTSGTAAAGCLVNDYPEPEVTWNSGALTSGVHTPPAV 175
DB 118 SASST--KGPSVFPPLAPSSKSTSGTAAAGCLVNDYPEPEVTWNSGALTSGVHTPPAV 175

Db 120 SSASTGKGPVPEPLAPSSKSTSGTALGCLVQDYPPEPVTVSMNSGALTSGVHTPAV 179
QY 176 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 235
Db 180 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 239
QY 236 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 295
Db 240 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 299
QY 296 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 355
Db 300 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTPTVLDSGDFLYSKLTV 415
Db 360 SRDELTKNQVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTPTVLDSGDFLYSKLTV 419
QY 416 KSRMOGNVFSQVMEHNLHNYTKSLSPGK 449
Db 420 KSRMOGNVFSQVMEHNLHNYTKSLSPGK 453

RESULT 7
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1 heavy chain
US-08-466-163B-8

Query Match 69.2%; Score 2124; DB 3; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.6e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;
QY 1 EYLVESGDFPVKPGSLKVCASGPAF-SHYAMSWVROTPAKRLEWVAIYSSGSGTY 59
Db 1 EYLVESGDFPVKPGSLKVCASGPAF-SHYAMSWVROTPAKRLEWVAIYSSGSGTY 59
QY 60 YSDSVGRFTISDNANKTLYLQMRSLRSEDSAMYFCTRYK--LGTVPFSDMGQTLTV 117
Db 60 YSDSVGRFTISDNANKTLYLQMRSLRSEDSAMYFCTRYK--LGTVPFSDMGQTLTV 117
QY 60 YADSVGRFTISDDSKNTFYLOMSLRADTAIVYICAGSHYFGMHFAVWGQGLTV 119
Db 60 YADSVGRFTISDDSKNTFYLOMSLRADTAIVYICAGSHYFGMHFAVWGQGLTV 119
QY 118 SSAST--KGPVPEPLAPSSKSTSGTALGCLVQDYPPEPVTVSMNSGALTSGVHTPAV 175
Db 120 SSASTKGPVPEPLAPSSKSTSGTALGCLVQDYPPEPVTVSMNSGALTSGVHTPAV 179
QY 176 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 235
Db 180 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 239
QY 236 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 295
Db 240 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 295

Db 240 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 299
QY 296 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 355
Db 300 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 359
QY 356 SRDELTKNQVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTPTVLDSGDFLYSKLTV 415
Db 360 SRDELTKNQVSLTCLVKGFPSPDIAVEMESNGOPENNYKTTPTVLDSGDFLYSKLTV 419
QY 416 KSRMOGNVFSQVMEHNLHNYTKSLSPGK 449
Db 420 KSRMOGNVFSQVMEHNLHNYTKSLSPGK 453

RESULT 8
US-09-802-096-8
; Sequence 8, Application US/09802096
; Patent No. 6685939
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3U5
; CURRENT APPLICATION NUMBER: US/09/802,096
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1 heavy chain
US-09-802-096-8

Query Match 69.2%; Score 2124; DB 4; Length 453;
Best Local Similarity 88.8%; Pred. No. 2.6e-157;
Matches 403; Conservative 21; Mismatches 24; Indels 6; Gaps 4;
QY 1 EYLVESGDFPVKPGSLKVCASGPAF-SHYAMSWVROTPAKRLEWVAIYSSGSGTY 59
Db 1 EYLVESGDFPVKPGSLKVCASGPAF-SHYAMSWVROTPAKRLEWVAIYSSGSGTY 59
QY 60 YSDSVGRFTISDNANKTLYLQMRSLRSEDSAMYFCTRYK--LGTVPFSDMGQTLTV 117
Db 60 YSDSVGRFTISDNANKTLYLQMRSLRSEDSAMYFCTRYK--LGTVPFSDMGQTLTV 117
QY 60 YADSVGRFTISDDSKNTFYLOMSLRADTAIVYICAGSHYFGMHFAVWGQGLTV 119
Db 60 YADSVGRFTISDDSKNTFYLOMSLRADTAIVYICAGSHYFGMHFAVWGQGLTV 119
QY 118 SSAST--KGPVPEPLAPSSKSTSGTALGCLVQDYPPEPVTVSMNSGALTSGVHTPAV 175
Db 120 SSASTKGPVPEPLAPSSKSTSGTALGCLVQDYPPEPVTVSMNSGALTSGVHTPAV 179
QY 176 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 235
Db 180 LOSGGLYSLSVTVTPSSSLGTOTYICNVNHHKPSNTVDKKVREKSCDKHTHCPCPAPE 239
QY 236 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 295
Db 240 LLAGPSVFLFPPPKOTLMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPRE 299
QY 296 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 355
Db 300 EGYNSTYRVVSVLTVLHQMNLNGEKYCKVSNKLPAPIEKTISKAGPREPOVYTLPP 359


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QY      418 RMOQGNVFSCSVHEALHNHYTKSLSPGK 449
         |||||
Db      420 RMOQGNVFSCSVHEALHNHYTKSLSPGK 451
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RESULT 11

```

US-08-887-352B-16
Sequence 16, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jarden, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-16

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Query Match	69.1%;	Score 2122;	DB 2;	Length 451;
Best Local Similarity	88.7%;	Pred. No. 3.7e-157;		
Matches 401; Conservative	21;	Mismatches 26;	Indels 4;	Gaps 3

Qy	1	EVTLVESGDDFYKPCGSLKLVSCAAGFAF-SHYAMSWNQTPAKRLREMAVLAISGGSGRY	59
Db	1	EVQLVESGGGLVQPGGSLRLSCAASGYSITISGYSMMIMQAPKQGLBEMVAISITIDDS-IN	59
Qy	60	YSDSYKGFITISRDAKNTLYIQMNSLRSEDSAMFCTRYK-LGTYIDDSWGCGTTLTY	117
Db	60	YNPSYKGRITISRDSKNTFYIQMNSLRBEDVAVYCAAGSHYFGHMHWAGCGTGLTY	119
Qy	118	SSASTKGRSVFPLAESSKTSGGTALGLVMDYPEEPTVSNVSGALNSGVATPAVQ	177
Db	120	SSASTKGRSVFPLAESSKTSGGTALGLVMDYPEEPTVSNVSGALNSGVATPAVQ	179
Qy	178	SSGLYSLSVYTVPESSLGTOYIICNVNHNKPSNTKYDKVYEPKSCKHTICPCAPPELL	237
Db	180	SSGLYSLSVYTVPESSLGTOYIICNVNHNKPSNTKYDKVYEPKSCKHTICPCAPPELL	239
Qy	238	GGPSVYFLPEPKQOTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQGVENAAATKPREQ	297
Db	240	GGPSVYFLPEPKQOTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDQGVENAAATKPREQ	299
Qy	298	YNSTRRVSVLTVLHQDWLNKGEYCKNSKALPAIEKTIISAKQOPPEPOVYTLPPSR	357
Db	300	YNSTRRVSVLTVLHQDWLNKGEYCKNSKALPAIEKTIISAKQOPPEPOVYTLPPSR	359

QY	358	DELTKNQVSLTCLVCKGFPSPDIAVWMSNGQENNNYKTTPEVLSDSGSFPLYSLVYDKS	417
Db	360	EMTKNQVSLTCLVCKGFPSPDIAVWMSNGQENNNYKTTPEVLSDSGSFPLYSLVYDKS	419
QY	418	RMOQGVNPSGVNHEALNNHYTKSLISLSPGK	449
Db	420	RMOQGVNPSGVNHEALNNHYTKSLISLSPGK	451

RESULT 12

US-08-466-151-65
Sequence 65, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM pc compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE: 1998-01-01

Query Match	69.1%	Score 2122	DB 3	Length 451
Best Local Similarity	88.7%	Score, No. 3.7e-157		
Matches 401	Conservative 21	Mismatches 26	Indels 4	Gaps 3

QY	1	E	V	T	L	V	E	S	G	G	D	F	P	K	P	G	C	S	L	K	V	C	A	A	G	A	R	-	S	H	A	M	S	W	R	O	P	R	A	R	L	E	M	A	V	I	S	G	G	C	T	V	59
DQ	1	E	V	O	L	V	E	S	G	G	G	L	V	O	P	G	S	L	K	V	C	A	A	G	A	R	-	S	H	A	M	S	W	R	O	P	R	A	R	L	E	M	A	V	I	S	G	G	C	T	V	59	
QY	60	Y	S	D	S	V	K	G	R	F	T	T	S	R	D	N	A	K	T	L	Y	O	M	S	L	R	S	E	D	S	A	M	-	P	C	T	R	V	K	-	L	G	T	Y	P	D	S	G	G	T	L	V	117
DQ	60	Y	S	D	S	V	K	G	R	F	T	T	S	R	D	N	A	K	T	L	Y	O	M	S	L	R	S	E	D	S	A	M	-	P	C	T	R	V	K	-	L	G	T	Y	P	D	S	G	G	T	L	V	117
QY	60	Y	N	P	S	V	N	G	R	T	T	I	R	D	S	K	T	F	L	O	N	N	S	L	A	E	D	T	A	V	Y	-	C	A	R	G	S	H	Y	E	G	N	H	F	A	V	M	O	G	T	L	V	119
DQ	60	Y	N	P	S	V	N	G	R	T	T	I	R	D	S	K	T	F	L	O	N	N	S	L	A	E	D	T	A	V	Y	-	C	A	R	G	S	H	Y	E	G	N	H	F	A	V	M	O	G	T	L	V	119

QY 118 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 177
DB 120 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 179
QY 178 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 237
DB 180 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 239
QY 238 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 297
DB 240 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 299
QY 298 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357
DB 300 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
QY 358 DELTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 417
DB 360 EEMTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 419
QY 418 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 449
DB 420 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 451

RESULT 13

US-09-109-207C-14
Sequence 14, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 3.7e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EYTLVSGGDPYKPGGSLKVSQASGPAF-SHYANSMVROTAPKRLWVAVYSSGSGSTY 59
DB 1 EYTLVSGGDPYKPGGSLKVSQASGPAF-SHYANSMVROTAPKRLWVAVYSSGSGSTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMVCTRVK--LGTYYFDSNGOGTTLV 117
DB 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMVCTRVK--LGTYYFDSNGOGTTLV 119
QY 118 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 177
DB 120 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 179
QY 178 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 237
DB 180 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 239
QY 238 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 297
DB 240 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 299

QY 298 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357
DB 300 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
QY 358 DELTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 417
DB 360 EEMTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 419
QY 418 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 449
DB 420 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 451

RESULT 14

US-09-109-207C-16
Sequence 16, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 3.7e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EYTLVSGGDPYKPGGSLKVSQASGPAF-SHYANSMVROTAPKRLWVAVYSSGSGSTY 59
DB 1 EYTLVSGGDPYKPGGSLKVSQASGPAF-SHYANSMVROTAPKRLWVAVYSSGSGSTY 59
QY 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMVCTRVK--LGTYYFDSNGOGTTLV 117
DB 60 YSDSVKGRFTISRDNKNTLYLQMSLRSEDSAMVCTRVK--LGTYYFDSNGOGTTLV 119
QY 118 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 177
DB 120 SSASTKGPSPVPLAPSSKSTSGTAAAGCLVNDYFPEPVTVSMNSGALTSGVHTFPAVLQ 179
QY 178 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 237
DB 180 SSGGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKHTHCPCPAPELL 239
QY 238 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 297
DB 240 GGPSPVFLPPPKKDTLMTISRPEVTCVVVDVSHEDPEVKFNNYVGVGHNAKTKPRREQ 299
QY 298 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 357
DB 300 YNSTYRVVSVLTVLHQMNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
QY 358 DELTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 417
DB 360 EEMTNQVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPVLDSDGSFPLYSKLTVDKS 419
QY 418 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 449
DB 420 RMQOGNVFSCSVMEALHNHYTOKSLSPGK 451

RESULT 15
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-14

Query Match 69.1%; Score 2122; DB 3; Length 451;
Best Local Similarity 88.7%; Pred. No. 3,7e-157;
Matches 401; Conservative 21; Mismatches 26; Indels 4; Gaps 3;

QY 1 EYTVESGGDFVKGSGSLKVCASAGFAF-SHYAMSVVROTPAKRLWVAYISSGSGTY 59
1 EVQLVDSGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGS-TN 59
DB 1 EVQLVDSGGGLVQPGGSLRLSCAASGYSITSGYSWMNIRQAPGKLEWVASITVDGS-TN 59
QY 60 YNSDVVGRFTISDNNNTLYLQMRSLRSDSAMFCTRVK--LGYTFPSMGCTLTLY 117
60 YNSDVVGRFTISDNNNTLYLQMRSLRSDSAMFCTRVK--LGYTFPSMGCTLTLY 117
DB 60 YNSDVVGRFTISDNNNTLYLQMRSLRSDSAMFCTRVK--LGYTFPSMGCTLTLY 117
QY 118 SSASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNVSGALTSVHTFPAVLQ 177
118 SSASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNVSGALTSVHTFPAVLQ 177
DB 120 SSASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNVSGALTSVHTFPAVLQ 179
120 SSASTKGPSPVPLAPSSKSTSGTALGCLVKDYFPEPVTVSNVSGALTSVHTFPAVLQ 179
QY 178 SSGLYSLSSVVTVPSSSLGTQYICNVNHRPSNTKYDKVPEKSCDKTHTCPPCPAPELL 237
178 SSGLYSLSSVVTVPSSSLGTQYICNVNHRPSNTKYDKVPEKSCDKTHTCPPCPAPELL 237
DB 180 SSGLYSLSSVVTVPSSSLGTQYICNVNHRPSNTKYDKVPEKSCDKTHTCPPCPAPELL 239
180 SSGLYSLSSVVTVPSSSLGTQYICNVNHRPSNTKYDKVPEKSCDKTHTCPPCPAPELL 239
QY 238 GGSVFLFPPKPRDTLMISRTPEVTCVVNVDSHEDPEVKFNWYVDGVEVNAKTKPREEQ 297
238 GGSVFLFPPKPRDTLMISRTPEVTCVVNVDSHEDPEVKFNWYVDGVEVNAKTKPREEQ 297
DB 240 GGSVFLFPPKPRDTLMISRTPEVTCVVNVDSHEDPEVKFNWYVDGVEVNAKTKPREEQ 299
240 GGSVFLFPPKPRDTLMISRTPEVTCVVNVDSHEDPEVKFNWYVDGVEVNAKTKPREEQ 299
QY 298 YNSTYRVSVLTLYLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPFSR 357
298 YNSTYRVSVLTLYLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPFSR 357
DB 300 YNSTYRVSVLTLYLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPFSR 359
300 YNSTYRVSVLTLYLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPFSR 359
QY 358 DELTKQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 417
358 DELTKQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 417
DB 360 EEMTKQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 419
360 EEMTKQVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 419
QY 418 RMQGNVVFSCSVNHEALHNHYTQKSLSLSPGK 449
418 RMQGNVVFSCSVNHEALHNHYTQKSLSLSPGK 449
DB 420 RMQGNVVFSCSVNHEALHNHYTQKSLSLSPGK 451
420 RMQGNVVFSCSVNHEALHNHYTQKSLSLSPGK 451

Search completed: December 23, 2004, 19:08:03
Job time : 39.4376 secs

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OM protein - protein search, using sw model

Run on: December 23, 2004, 19:04:51 / Search time 132.396 Seconds
(Without alignments)
1578.640 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVESGDFVKGSLKV.....IVEFLRNWTFQSIISTLT 582

Scoring table:

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Gapop 10.0, Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubppa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubppa/US09C_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubppa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubppa/US10D_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2744.5	89.4	579	US-10-138-727A-41	Sequence 41, App1
2	2738.5	89.2	579	US-10-310-719-32	Sequence 32, App1
3	2715.5	88.4	575	US-10-737-208A-6	Sequence 6, App1
4	2592	83.4	580	US-10-310-719-37	Sequence 37, App1
5	2560	83.4	580	US-10-310-719-35	Sequence 35, App1
6	2218.5	72.2	663	US-10-412-406-32	Sequence 32, App1
7	2218.5	72.2	4852	US-10-412-406-33	Sequence 33, App1
8	2216	72.2	713	US-10-679-620-64	Sequence 64, App1
9	2216	72.2	715	US-10-679-620-62	Sequence 62, App1
10	2201.5	71.7	447	US-10-474-832-4	Sequence 4, App1
11	2200.5	71.7	444	US-10-150-475A-6	Sequence 6, App1
12	2200.5	71.7	444	US-10-704-522-6	Sequence 6, App1
13	2200.5	71.7	444	US-10-645-215-6	Sequence 6, App1

14	2197	71.5	449	US-10-635-908-16	Sequence 16, App1
15	2197	71.5	449	US-10-635-908-18	Sequence 18, App1
16	2195.5	71.5	445	US-10-320-231A-79	Sequence 79, App1
17	2195.5	71.5	447	US-10-474-832-5	Sequence 5, App1
18	2191.5	71.4	446	US-10-474-832-6	Sequence 6, App1
19	2184.5	71.1	446	US-10-408-901-38	Sequence 38, App1
20	2181	71.0	449	US-09-736-371B-21	Sequence 21, App1
21	2181	71.0	449	US-10-463-442-21	Sequence 21, App1
22	2181	71.0	474	US-09-848-832-3	Sequence 3, App1
23	2181	71.0	474	US-10-225-108A-3	Sequence 3, App1
24	2177.5	70.9	442	US-10-461-148-1	Sequence 1, App1
25	2177.5	70.9	442	US-10-226-435A-12	Sequence 12, App1
26	2177.5	70.9	442	US-10-487-326-12	Sequence 12, App1
27	2177.5	70.9	442	US-10-486-908-12	Sequence 12, App1
28	2177.5	70.9	447	US-10-291-265-395	Sequence 395, App1
29	2176	70.9	445	US-10-408-901-34	Sequence 34, App1
30	2171	70.7	451	US-09-822-698A-26	Sequence 26, App1
31	2170.5	70.7	442	US-10-487-326-12	Sequence 12, App1
32	2170.5	70.7	442	US-10-487-326-12	Sequence 12, App1
33	2170.5	70.7	442	US-10-486-908-16	Sequence 16, App1
34	2166.5	70.5	446	US-10-408-901-46	Sequence 46, App1
35	2166.5	70.5	469	US-10-858-186-14	Sequence 14, App1
36	2159.5	70.3	446	US-10-408-901-30	Sequence 30, App1
37	2159	70.3	445	US-10-408-901-42	Sequence 42, App1
38	2158.5	70.1	446	US-10-408-901-50	Sequence 50, App1
39	2153.5	70.1	469	US-10-656-769-26	Sequence 26, App1
40	2152	70.1	474	US-10-108-260A-4640	Sequence 4640, App1
41	2149.5	69.9	452	US-09-726-258-71	Sequence 71, App1
42	2147.5	69.9	469	US-10-656-769-20	Sequence 20, App1
43	2145.5	69.9	447	US-10-379-392-116	Sequence 116, App1
44	2145.5	69.9	452	US-10-818-765-4	Sequence 4, App1
45	2144.5	69.8	447	US-10-379-392-117	Sequence 117, App1

ALIGNMENTS

RESULT 1

US-10-138-727A-41

Sequence 41, Application US/10138727A

Publication No. US20030157054A1

GENERAL INFORMATION:

APPLICANT: Gillies, Stephen

APPLICANT: Lo, Kin-Ming

FILE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof

FILE REFERENCE: LEX-019

CURRENT APPLICATION NUMBER: US/10/138, 727A

CURRENT FILING DATE: 2002-05-03

PRIOR APPLICATION NUMBER: US 60/288, 564

PRIOR FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 579

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: heavy chain-III2

US-10-138-727A-41

Query Match 89.4% Score 2744.5; DB 14; Length 579;

Best Local Similarity 88.5% Pred. No. 1.4e-166;

Matches 516; Conservative 31; Mismatches 31; Indels 5; Gaps 2;

QY 1 EVTLVESGDFVKGSLKVCASGPAFHYAMSWROTAPKRLVAVYISGSGSTYY 60

1 QIQLVGSAGVKKPGEVYKSCASGTFYNNYGAMWKQIPGGLKMMGINTYTGPT 60

DB 61 SDVSKGFTTIRDNKNTLYLQKSLRSEDSDAMVFCFTR-VKLGTYYFDSNGCGTTLVSS 119

DB 61 ADPKGRFARSLSTSTATLQINNLRSBDTATYFCVRFYSKDY----WGQGSYTVSS 116

QY	120	ASTKBPSPFLA	BSKSN	SGTAAG	GLCVKQV	PREPVYU	SMSGALT	SGVHN	PPAYLOSS	179		
Db	117	ASTKBPSPFLA	BSKSN	SGTAAG	GLCVKQV	PREPVYU	SMSGALT	SGVHN	PPAYLOSS	176		
QY	180	GLYLSLSVYTV	VBSSSL	IGTQTY	ICNVHNK	SPSNK	KVDKKV	PPKSCDK	NKHTCP	PCAPBELLGG	239	
Db	177	GLYLSLSVYTV	VBSSSL	IGTQTY	ICNVHNK	SPSNK	KVDKRVP	PKSCDK	NKHTCP	PCAPBELLGG	236	
QY	240	PSVFLFP	PREPKDTLMI	SRTPEV	YTCVYVDV	SHEDPEV	KFMVYVDG	VEVHN	AKTYPREBOYN	239		
Db	237	PSVFLFP	PREPKDTLMI	SRTPEV	YTCVYVDV	SHEDPEV	KFMVYVDG	VEVHN	AKTYPREBOYN	236		
QY	300	STYRVVSVLTV	LHODMLN	KEKYCK	KVSNKAL	PAP	IEKITS	SKAKG	CPREPOVYTL	PPESRDE	359	
Db	297	STYRVVSVLTV	LHODMLN	KEKYCK	KVSNKAL	PAP	IEKITS	SKAKG	CPREPOVYTL	PPESRDE	356	
QY	360	LTKNOVSL	CTLCKVGFY	PSDIA	VEWESN	GCP	PENNYK	TPPVL	VDSDGSP	FLYSKULTVDKSRW	419	
Db	357	MTKNQVSL	CTLCKVGFY	PSDIA	VEWESN	GCP	PENNYK	TPPVL	VDSDGSP	FLYSKULTVDKSRW	416	
QY	420	OOGANV	FSCSVMBE	ALHNHTOK	SLSPK	APSS	TKTKTOU	QLEHLL	LDLOU	TLNGINN	479	
Db	417	OOGANV	FSCSVMBE	ALHNHTOK	SLSPK	APSS	TKTKTOU	QLEHLL	LDLOU	TLNGINN	476	
QY	480	YKNPPL	LTMLTFK	FYMPK	KATBLKHL	QCL	EEBLK	XP	EEVYLAN	AOSKNFHLRP	PDLSINN	539
Db	477	YKNPPL	LTMLTFK	FYMPK	KATBLKHL	QCL	EEBLK	XP	EEVYLAN	AOSKNFHLRP	PDLSINN	536
QY	540	VIVLELK	GSSETTFM	CEBYADE	TAETATY	VEFLNR	MIT	FCOS	II	STULT	562	
Db	537	VIVLELK	GSSETTFM	CEBYADE	TAETATY	VEFLNR	MIT	FCOS	II	STULT	579	

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RESULT 2
US-10-310-719-32
; Sequence 32, Application US/10310719
; Publication No. US2003016615A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-KS-ala IL2 (D20T) heavy chain fused to IL-2 variant
US-10-310-719-32

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[illegible][illegible]

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RESULT 3
US-10-737-208A-6
; Sequence 6, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin Heavy Chain-IL-2
US-10-737-208A-6

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[illegible]


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Db 235 SVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREBOYN 294
Qy 301 TYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSDEL 360
Db 295 TYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSHEEM 354
Qy 361 TKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Db 355 TKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 414
Qy 421 QGNVSCSVMAHNLHNYTQKSLSPGKAPTSSTTKTQLOLEHLLDLMILNGINNY 480
Db 415 QGNVSCSVMAHNLHNYTQKSLSPGKAPTSSTTKTQLOLEHLLDLMILNGINNY 473
Qy 481 KNPCLTRMLTPKFPYMPKATELKHLOCLEBEELKPLEEVNLAKSKNPHLRPRDLISINV 540
Db 474 KNPCLTRMLTPKFPYMPKATELKHLOCLEBEELKPLEEVNLAKSKNPHLRPRDLISINV 533
Qy 541 VIVLEKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
Db 534 VIVLEKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 575
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RESULT 4
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; LENGTH: 580
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76 (gamma4h) (FN-AQ)-ala-IL2 (D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37
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Query Match 84.4%; Score 2592; DB 14; Length 580;
Best Local Similarity 84.7%; Pred. No. 7.1e-157;
Matches 494; Conservative 31; Mismatches 54; Indels 4; Gaps 3;

Qy 1 EYTLVSGDGFVKPGGSLKVCSCASGFAFSH-YAMSWVROTPAKRLWVAYISSGSGTY 59
Db 1 QVQLOESGPGVLVPRSETLSLTCAVSGYSSISGYWGIROPKGLWISGSIYHSGS-TY 59
Qy 60 YSDSVKGRFTISRDNANKTLYLQMRSLRSDSAMYFCTRYKLGATYYFSDSWGQGTTLTVSS 119
Db 60 YNPSLKSRTVITSVDTSKNQFSLKLSSTVADTAVYCARGKWSK--FDYWGQGLTVLVSS 117
Qy 120 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
Db 118 ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
Qy 180 GLVSLSSVTVTPSSSLGTTQTYICNVNKKPSNTKVDKVPKSCDKHTHCPCPAPRLG 239
Db 178 GLVSLSSVTVTPSSSLGTTQTYICNVNKKPSNTKVDKVPKSCDKHTHCPCPAPRLG 237
Qy 240 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREBOYN 299
Db 238 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREBOAQ 297
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Qy 300 STYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 359
Db 298 STYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSQDE 357
Qy 360 LTRNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 419
Db 358 MTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 417
Qy 420 QGNVSCSVMAHNLHNYTQKSLSPGKAPTSSTTKTQLOLEHLLDLMILNGINNY 479
Db 418 QGNVSCSVMAHNLHNYTQKSLSPGKAPTSSTTKTQLOLEHLLDLMILNGINNY 477
Qy 480 KNPCLTRMLTPKFPYMPKATELKHLOCLEBEELKPLEEVNLAKSKNPHLRPRDLISIN 539
Db 478 KNPCLTRMLTPKFPYMPKATELKHLOCLEBEELKPLEEVNLAKSKNPHLRPRDLISIN 537
Qy 540 VIVLEKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 582
Db 538 VIVLEKGETTFMCEYADETATVEFLNRWITFCQSIISTLT 580
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RESULT 5
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; LENGTH: 580
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76 (gamma2h) (FN-AQ)-ala-IL2 (D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
US-10-310-719-35
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Query Match 83.4%; Score 2560; DB 14; Length 580;
Best Local Similarity 84.1%; Pred. No. 7.8e-155;
Matches 491; Conservative 31; Mismatches 56; Indels 6; Gaps 5;

Qy 1 EYTLVSGDGFVKPGGSLKVCSCASGFAFSH-YAMSWVROTPAKRLWVAYISSGSGTY 59
Db 1 QVQLOESGPGVLVPRSETLSLTCAVSGYSSISGYWGIROPKGLWISGSIYHSGS-TY 59
Qy 60 YSDSVKGRFTISRDNANKTLYLQMRSLRSDSAMYFCTRYKLGATYYFSDSWGQGTTLTVSS 119
Db 60 YNPSLKSRTVITSVDTSKNQFSLKLSSTVADTAVYCARGKWSK--FDYWGQGLTVLVSS 117
Qy 120 -ASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 178
Db 118 GASTKGPSVPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 177
Qy 179 SGLVSLSSVTVTPSSSLGTTQTYICNVNKKPSNTKVDKVPKSCDKHTHCPCPAPRLG 238
Db 178 SGLVSLSSVTVTPSSSLGTTQTYICNVNKKPSNTKVDKVPKSCDKHTHCPCPAPRLG 236
Qy 239 GPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREBOY 298
Db 237 GPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVNAKTKPREBOA 296
Qy 299 NSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 358
Db 297 NSTYRVSVLTVLHODMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 356
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Qy	359	LTTRNQVSLCTLYGFGYSDIAVEMESNGOENNKTTPVLDSGSEFLYSKLVYDKSR	418
Db	357	ETRNQVSLCTLYGFGYSDIAVEMESNGOENNKTTPVLDSGSEFLYSKLVYDKSR	416
Qy	419	WQGVNFSVCSVMHEALHNHYTOKSLSPGKAPTSSTSTKTKTQLOLEHLLLDLOMLINGIN	478
Db	417	WQGVNFSVCSVMHEALHNHYTOKSATATPGAAPTSSTTKTKTQLOLEHLLLDLOMLINGIN	476
Qy	479	NYKPKLTRMTTFKRYMPKKATTELKHOCLBEELKPLLEEVNLAOSKNPHLRPRLISNI	538
Db	477	NYKPKLTRMTTFKRYMPKKATTELHGOCLBEELPLLEEVNLAOSKNPHLRPRLISNI	536
Qy	539	NYVLELKGSETTFMCEYADETATIVETPLNMTFCOSIISTLT	582
Db	537	NYVLELKGSETTFMCEYADETATIVETPLNMTFCOSIISTLT	580
RESULT 6			
US-10-412-406-32			
Sequence 32, Application US/10412406			
Publication No. US20040058394A1			
GENERAL INFORMATION:			
APPLICANT: BIOGEN, INC.			
APPLICANT: GARBER, Ellen			
APPLICANT: LYNE, Paul			
APPLICANT: SALDHANA, Jose W.			
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES			
FILE REFERENCE: BINA100CN			
CURRENT APPLICATION NUMBER: US/10/412,406			
CURRENT FILING DATE: 2003-04-10			
PRIOR APPLICATION NUMBER: 60/240,285			
PRIOR FILING DATE: 2000-10-13			
PRIOR APPLICATION NUMBER: 60/275,289			
PRIOR FILING DATE: 2001-03-13			
PRIOR APPLICATION NUMBER: 60/299,987			
PRIOR FILING DATE: 2001-06-21			
PRIOR APPLICATION NUMBER: PCT/US01/32140			
PRIOR FILING DATE: 2001-10-12			
NUMBER OF SEQ ID NOS: 33			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 32			
LENGTH: 663			
TYPE: PRT			
ORGANISM: Homo Sapien			
US-10-412-406-32			
Query Match 72.2%; Score 2218.5; DB 15; Length 663;			
Best Local Similarity 93.1%; Pred. No. 5,2e-133;			
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1.			
Qy	1	EVTLVESGDDFFKPGGSLKVSQASGAFPSHAMSVMQTPAKRLIEWAVYISSGGSGTY	60
Db	215	EVQLVESGGGLVKKPGGSLRLISQASGFFTFSDYIMWFQAPGKGLIEWAITSDDGSYTY	274
Qy	61	SDSVKGRFTISRDAKNTLYIQMRSLSRSEDSAMYPECTVRLKGT-YYPSWGGITLTYS	119
Db	275	PDSVYGRFTISRDAKNSLYIQMSLSRAEDTAVYYCAAEENGNNFYYPYWGQGITTVTSS	334
Qy	120	ASTKGPSTFPLAPSSKSTISGTAALGCLVKDYFPEPTVYSNWSGALTISGAVTFPAVLOS	179
Db	335	ASTKGPSVFPLAPSSKSTISGTAALGCLVKDYFPEPTVYSNWSGALTISGAVTFPAVLOS	394
Qy	180	GLYSLSVWVWPPSSSLGTQTYICNNNHKPSNTKVDKVEPSCDTHTHCPCPAPAEELGG	239
Db	395	GLYSLSVWVWPPSSSLGTQTYICNNNHKPSNTKVDKVEPSCDTHTHCPCPAPAEELGG	454
Qy	240	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKRWYDVGVEVHNAAKTRPEEYOYN	299
Db	455	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKRWYDVGVEVHNAAKTRPEEYOYN	514
Qy	300	STYRVASVLTYLHQDWLNGKEYKCKVSNKALPAPIEKITISRAKGGPREPQVYITLPPSRDE	359

Db	515	STRVSVLVLTVYHQDMLNGKEVCKKSNKALPAPIEKTISKAGQGPPEPVYTLPPSRDE	574
Qy	360	LTKNQVSLTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKULTVDKSRW	419
Db	575	LTKNQVSLTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKULTVDKSRW	634
Qy	420	QQGNVFCSCVMHEALHNHYTQKSLSLSPG	448
Db	635	QQGNVFCSCVMHEALHNHYTQKSLSLSPG	663
RESULT 7			
US-10-412-406-33			
; Sequence 33, Application US/10412406			
; Publication No. US20040058394A1			
; GENERAL INFORMATION:			
; APPLICANT: BIOGEN, INC.			
; APPLICANT: GARBER, Ellen			
; APPLICANT: LYNE, Paul			
; APPLICANT: SALDHANA, Jose W.			
; TITLE OF INVENTION: HUMANIZED ANTI-LT-BEFA-R ANTIBODIES			
; FILE REFERENCE: BINAL00CN			
; CURRENT APPLICATION NUMBER: US/10/412,406			
; CURRENT FILING DATE: 2003-04-10			
; PRIOR APPLICATION NUMBER: 60/240,285			
; PRIOR FILING DATE: 2000-10-13			
; PRIOR APPLICATION NUMBER: 60/275,289			
; PRIOR FILING DATE: 2001-03-13			
; PRIOR APPLICATION NUMBER: 60/299,987			
; PRIOR FILING DATE: 2001-06-21			
; PRIOR APPLICATION NUMBER: PCT/US01/32140			
; PRIOR FILING DATE: 2001-10-12			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 33			
; LENGTH: 4852			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
US-10-412-406-33			
Query Match 72.2%; Score 2218.5; DB 15; Length 4852;			
Best Local Similarity 93.1%; Pred. No. 5,4e-132;			
Matches 418; Conservative 9; Mismatches 21; Indels 1; Gaps 1;			
Qy	1	EVTLVESGSDPVFKGGSLKVSCAASGFASHYAMSVWVQTQPAKRLLEVAVYISSGSGCTYY	60
Db	4404	EVQLVESGGGLVFRKGSGSLRLSCAASGTFSDYVYWFRAQPAKGLLEWATISDGSSTYY	4463
Qy	61	SDSYKRGFTISRDNKNTYTLQKRLSLEBSNMYFCIRVYLGT-YYPSMGCGCTTLTVSS	119
Db	4464	PDSTYKRGFTISRDNKNSLYLQMSLEAEDTAVYYCARENGNFYFDYVGGQCTTVSS	4523
Qy	120	ASTGSPVFPAPLAPSKSTSGGTALGCLVNDYFPEPYTVMNSGALTSGVHTFPALVQSS	179
Db	4524	ASTGSPVFPAPLAPSKSTSGGTALGCLVNDYFPEPYTVMNSGALTSGVHTFPALVQSS	4583
Qy	180	GLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVBEKSCDKHTCPCPAPELLGG	239
Db	4584	GLYSLSSVTVVPSSSLGTQTYICNVNHPKPSNTKVDKKVBEKSCDKHTCPCPAPELLGG	4643
Qy	240	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVYDGVENHNAKTYPRREQYN	299
Db	4644	PSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVYDGVENHNAKTYPRREQYN	4703
Qy	300	STRVSVLVLTVYHQDMLNGKEVCKKSNKALPAPIEKTISKAGQGPPEPVYTLPPSRDE	359
Db	4704	STRVSVLVLTVYHQDMLNGKEVCKKSNKALPAPIEKTISKAGQGPPEPVYTLPPSRDE	4763
Qy	360	LTKNQVSLTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKULTVDKSRW	419
Db	4764	LTKNQVSLTCLVKGFFYPSDIAVEMESNGQPENNYKTTTPVLDSGSPFLYSKULTVDKSRW	4823
Qy	420	QQGNVFCSCVMHEALHNHYTQKSLSLSPG	448

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: polypeptide
US-10-474-832-4

Query Match 71.7%; Score 2201.5; DB 15; Length 447;
Best Local Similarity 92.9%; Pred. No. 4e-132;
Matches 416; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY 1 EYLVESGGDFVYKPGSLKVCASGAFSHYAMSWVRQTPAKRLLEWVAIYSSGSGTTY 60
DB 1 EYLVESGGGLVYKPGSLKVCASGAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 59
QY 61 SDVSKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 120
DB 60 LBSVKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 119
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 180
DB 120 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 179
QY 181 LYSLSVTVVPSSSLGTQTYICNVNHPKPNNTKVDKVEPKSCDKHTTCCPCAPPELLGCP 240
DB 180 LYSLSVTVVPSSSLGTQTYICNVNHPKPNNTKVDKVEPKSCDKHTTCCPCAPPELLGCP 239
QY 241 SVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHNAKTKPREQYNS 300
DB 240 SVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHNAKTKPREQYNS 299
QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 360
DB 300 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 359
QY 361 TRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSRMQ 420
DB 360 TRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSRMQ 419
QY 421 QGNVFCSCVMEALHNHYTQKSLSPG 448
DB 420 QGNVFCSCVMEALHNHYTQKSLSPG 447

RESULT 11
US-10-150-475A-6
Sequence 6, Application US/10150475A
Publication No. US20030103985A1
GENERAL INFORMATION:
APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates
FILE REFERENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Humanised
OTHER INFORMATION: Murine Antibody BiMA 4 Heavy Chain Seq ID NO: 6
US-10-150-475A-6

Query Match 71.7%; Score 2200.5; DB 14; Length 444;
Best Local Similarity 92.4%; Pred. No. 4.6e-132;
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;
QY 1 EYLVESGGDFVYKPGSLKVCASGAFSHYAMSWVRQTPAKRLLEWVAIYSSGSGTTY 60
DB 1 EYLVESGGGLVYKPGSLKVCASGAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60

QY 61 SDVSKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 120
DB 61 LBSVKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 115
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 180
DB 116 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 175
QY 181 LYSLSVTVVPSSSLGTQTYICNVNHPKPNNTKVDKVEPKSCDKHTTCCPCAPPELLGCP 240
DB 176 LYSLSVTVVPSSSLGTQTYICNVNHPKPNNTKVDKVEPKSCDKHTTCCPCAPPELLGCP 235
QY 241 SVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHNAKTKPREQYNS 300
DB 236 SVFLPFPKPKDITLMISRTPEVTCVVDVSHEDPEVFNMYVDGVEVHNAKTKPREQYNS 295
QY 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 360
DB 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDEL 355
QY 361 TRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSRMQ 420
DB 356 TRKQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYSKLTVDSRMQ 415
QY 421 QGNVFCSCVMEALHNHYTQKSLSPG 449
DB 416 QGNVFCSCVMEALHNHYTQKSLSPG 444

RESULT 12
US-10-704-522-6
Sequence 6, Application US/10704522
Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Gunther
APPLICANT: Baumann, Michael
TITLE OF INVENTION: Compositions and methods for treating cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates
FILE REFERENCE: 1/1414
CURRENT APPLICATION NUMBER: US/10/704,522
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanised Murine Antibody BiMA 4 Heavy Chain
US-10-704-522-6

Query Match 71.7%; Score 2200.5; DB 16; Length 444;
Best Local Similarity 92.4%; Pred. No. 4.6e-132;
Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 EYLVESGGDFVYKPGSLKVCASGAFSHYAMSWVRQTPAKRLLEWVAIYSSGSGTTY 60
DB 1 EYLVESGGGLVYKPGSLKVCASGAFSHYAMSWVRQAPGKLEWVAIYSSGSGTTY 60
QY 61 SDVSKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 120
DB 61 LBSVKRFTISRDNANKNTLYLQMRSLRSEDSAMYFCTRVGLGTYFPDSMGQTTLLTVSSA 115
QY 121 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 180
DB 116 STKGPSVFPPLAPSSKSTSGGTAALGCLVNDYFPEPYTVSWNSGALTSVHTTTPAVLQSSG 175
QY 181 LYSLSVTVVPSSSLGTQTYICNVNHPKPNNTKVDKVEPKSCDKHTTCCPCAPPELLGCP 240

Db 176 LYSLSVTVTPSSSLGQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPBELGGP 235
Qy 241 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 300
Db 236 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 295
Qy 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355
Qy 361 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Db 356 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 415
Qy 421 QGNVFCSCVMHEALHNHYTKSLSPGK 449
Db 416 QGNVFCSCVMHEALHNHYTKSLSPGK 444

RESULT 13

US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; FILE REFERENCE: 1/1393
; CURRENT APPLICATION NUMBER: US/10/645, 215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody Biwa 4 Heavy Chain
US-10-645-215-6

Query Match 71.7%; Score 2200.5; DB 16; Length 444;

Best Local Similarity 92.4%; Pred. No. 4.6e-132;

Matches 415; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

Qy 1 EYTLVSGGDFVFKGSLKVCASGAFASHYAMSVWRQTPAKLEWVAIYSSGSGTYY 60
Db 1 EVOLVEGGGGLVKGSLRLSCASGFTFSSYDMSWRQAPGKLEWVSTISSGSGTYY 60
Qy 61 SDSVKGFTISRDNKNTLYLQMSLSRSDSAMYFCRTVRLGTYYPSPWGGTTLTVSSA 120
Db 61 LDSIKGFTISRDNKNTLYLQMSLSRSDSAMYFCRTVRLGTYYPSPWGGTTLTVSSA 115
Qy 121 STKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNWGSALTSGLVHTFPAVLQSSG 180
Db 116 STKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNWGSALTSGLVHTFPAVLQSSG 175
Qy 181 LYSLSVTVTPSSSLGQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPBELGGP 240
Db 176 LYSLSVTVTPSSSLGQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPBELGGP 235
Qy 241 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 300
Db 236 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 295
Qy 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360

Db 296 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 355
Qy 361 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Db 356 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 415
Qy 421 QGNVFCSCVMHEALHNHYTKSLSPGK 449
Db 416 QGNVFCSCVMHEALHNHYTKSLSPGK 444

RESULT 14

US-10-635-908-16
; Sequence 16, Application US/10635908
; Publication No. US20040219633A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer, Volker
; APPLICANT: Moehle, Thorsten
; TITLE OF INVENTION: Method of Producing Recombinant Antibodies
; FILE REFERENCE: 2923-552
; CURRENT APPLICATION NUMBER: US/10/635, 908
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: PCT/EP02/01283
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/327, 008
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/266, 853
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mouse anti-human monoclonal antibody
US-10-635-908-16

Query Match 71.5%; Score 2197; DB 17; Length 449;

Best Local Similarity 92.2%; Pred. No. 7.8e-132;

Matches 414; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EYTLVSGGDFVFKGSLKVCASGAFASHYAMSVWRQTPAKLEWVAIYSSGSGTYY 60
Db 1 EVOLVEGGGGLVKGSLRLSCASGFTFSSYDMSWRQAPGKLEWVSTISSGSGTYY 60
Qy 61 SDSVKGFTISRDNKNTLYLQMSLSRSDSAMYFCRTVRLGTYYPSPWGGTTLTVSSA 120
Db 61 LDSIKGFTISRDNKNTLYLQMSLSRSDSAMYFCRTVRLGTYYPSPWGGTTLTVSSA 120
Qy 121 STKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNWGSALTSGLVHTFPAVLQSSG 180
Db 121 STKGPVSFPLAPSSKSTSGTALGCLVKDYFPEPVTVSNWGSALTSGLVHTFPAVLQSSG 180
Qy 181 LYSLSVTVTPSSSLGQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPBELGGP 240
Db 181 LYSLSVTVTPSSSLGQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPBELGGP 240
Qy 241 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 300
Db 241 SVFLPPPKPDOTLMISRTPEVTCVVDVSHEDPEVKFVWYDGVYVNAKTKPREEOYNS 300
Qy 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Db 301 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 360
Qy 361 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Db 361 TKQVSLITCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQ 420
Qy 421 QGNVFCSCVMHEALHNHYTKSLSPGK 449

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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:46:03 ; Search time 31.449 Seconds

(without alignments)
1780.604 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071
Sequence: 1 EVTLVESGDFVKRSGSLKV.....IVEFLANRWTFQSIISTLT 582

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	57.5	330	1 GHNU	Ig gamma-1 chain C
2	1630.5	53.1	377	2 A2351.1	Ig gamma-3 chain C
3	1628.5	53.0	377	2 A60764	Ig gamma-3 chain C
4	1604	52.2	326	1 G2HU	Ig gamma-2 chain C
5	1590.5	51.8	327	1 G4HU	Ig gamma-4 chain C
6	1507.5	49.1	444	2 PC4436	monoclonal antibod
7	1466	47.7	470	2 S22080	Ig heavy chain pre
8	1430.5	46.6	469	2 S37483	Ig gamma-2a chain
9	1423	46.3	374	2 S69339	Ig heavy chain V r
10	1421	46.3	446	2 S40295	Ig gamma-2a chain
11	1412	46.0	472	2 S31459	Ig gamma-1 chain -
12	1365	44.4	474	1 G2MS11	Ig gamma-2b chain
13	1343.5	43.7	475	2 S01321	Ig gamma-2b chain
14	1263	41.1	328	2 147159	Ig gamma-2a chain
15	1260	41.0	325	2 S31866	Ig gamma-1 chain C
16	1257	40.9	328	2 147160	Ig gamma-2b chain
17	1254	40.8	234	2 PT0207	Ig gamma-2b chain
18	1231	40.1	328	2 147158	Ig gamma-1 chain C
19	1230.5	40.1	323	1 GHRB	Ig gamma-1 chain C
20	1227	40.0	328	2 147161	Ig gamma-3 chain C
21	1216.5	39.6	329	1 G2GP	Ig gamma-2 chain C
22	1161.5	37.8	308	2 C30554	Ig heavy chain C r
23	1152	37.5	326	2 PS0017	Ig gamma-1 chain C
24	1151	37.5	329	1 G3HWT	Ig gamma-1 chain C
25	1146.5	37.3	333	2 PS0018	Ig gamma-2b chain
26	1142	37.2	324	1 G1MS	Ig gamma-1 chain C
27	1141	37.2	329	1 G1MSC	Ig gamma-3 chain C
28	1139	37.1	393	1 G1MSM	Ig gamma-1 chain C
29	1130	36.8	398	1 G3MSM	Ig gamma-3 chain C

30	1126	36.7	330	1 G2MSA	Ig gamma-2a chain
31	1123.5	36.6	335	1 G2MSAB	Ig gamma-2a chain
32	1121	36.5	399	1 G2MSAM	Ig gamma-2a chain
33	1118.5	36.4	329	2 S00847	Ig gamma-2c chain
34	1118	36.4	548	2 S38864	Ig epsilon chain C
35	1112	36.2	322	2 PS0019	Ig gamma-2a chain
36	1092.5	35.6	327	2 S06611	Ig gamma-2 chain C
37	1082	35.2	405	1 G2MSBM	Ig gamma-2b chain
38	1066	34.7	277	2 147162	Ig gamma-4 chain C
39	845.5	27.5	549	2 S04845	Ig heavy chain pre
40	817.5	26.6	249	2 S69340	Ig heavy chain VHI
41	802.5	26.1	572	2 B46529	Ig Y heavy chain (
42	801.5	26.1	241	2 S69131	Ig heavy chain (DO
43	770	25.1	218	2 A35040	Ig heavy chain V-I
44	760	24.7	220	2 A49444	Ig gamma-1 heavy c
45	744.5	24.2	254	2 B31790	Ig heavy chain V r

ALIGNMENTS

RESULT 1

GHNU
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R/Elliason, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; PMID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <EHL>
A/Cross-references: UNIPROT:P01857; EMBL:Z17370
A/Note: this sequence has the Gln(17) alloctytic marker, 97-Lys, and the Gln(1) markers, R/Harris, L.J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: EMBL:Z17370
R/Takahashi, N.; Ueda, S.; Obata, M.; Nakaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A/Reference number: S33887; PMID:83001943; PMID:681139
A/Accession: S33887
A/Molecule type: DNA
A/Residues: 88-113;235-330 <TAK>
A/Cross-references: EMBL:Z17370
R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seque
A/Reference number: A90563; PMID:71064024; PMID:5489771
A/Accession: B90563
A/Molecule type: protein
A/Residues: 1-96, 'R', 98-135 <GUN>
R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ
A/Reference number: A90564; PMID:71064025; PMID:5530842
A/Accession: A90564
A/Molecule type: protein
A/Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240
A/Note: this sequence has the Gln(tron-1) markers, 239-Glu and 241-Met
R/Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle).

F:20-85/Domain: immunoglobulin homology <IM>

Query Match 53.0%; Score 1628.5; DB 2; Length 377;
 Best Local Similarity 82.0%; Pred. No. 1.9e-84;
 Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

Qy 120 ASTKPSFPLAPBSKSTSGTAAAGCLVXDYFPEPVVSNWNGALTSGVTFPAVLQSS 179
 Db 1 ASTGSPFPLAPBSKSTSGTAAAGCLVXDYFPEPVVSNWNGALTSGVTFPAVLQSS 60

Qy 180 GLYSLSSVTVVPSSSLGTQYICVNHKPSNTKYDKV----- 217
 Db 61 GLYSLSSVTVVPSSSLGTQYICVNHKPSNTKYDKVELKTPGLDTHTCPCRCPEKSC 120

Qy 218 -----EPKSCKTHTCPCRCPEKSCPELLGGSVTLFPKPKDT 252
 Db 121 DTPPCPCRCPEKSCPTPPPCRCPEKSCPTPPPCPCAPPELLGGSVTLFPKPKDT 180

Qy 253 LMIKRTPEVTCVVDVSHEDPEVKNVYDGVENHNAKTRERQYNSTYRVVSVLTVLH 312
 Db 181 LMIKRTPEVTCVVDVSHEDPEVQKMYVDGVEVHNAKTRERQYNSTYRVVSVLTVLH 240

Qy 313 QDWLNGEKYCKVSNKALPAPIEKTISKAKQPREPVYTLPPSRDELTKNQVSLTCLVK 372
 Db 241 QDWLNGEKYCKVSNKALPAPIEKTISKAKQPREPVYTLPPSRDEWTKNQVSLTCLVK 300

Qy 373 GFYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGVNFGCSVWHE 432
 Db 301 GFYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQGVNFGCSVWHE 360

Qy 433 ALHNHYTKSLSLSPGK 449
 Db 361 ALHNHYTKSLSLSPGK 377

RESULT 4

G2HU

Ig gamma-2 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004

C:Accession: A93906; A92809; A90752; A93132; A02148

R:Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain c

A:Reference number: A93906; MUID:82197621; PMID:6804948

A:Accession: A93906

A:Molecule type: DNA

A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; F

A:Note: Lys-326 is probably removed posttranslationally

R:Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A:Reference number: A92809; MUID:81007873; PMID:6774012

A:Accession: A92809

A:Molecule type: protein

A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>

A:Note: Tyr-156 is at or near the complement-binding site

R:Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A:Title: The amino acid sequences of the three heavy chain constant region domains of a

A:Reference number: A90752; MUID:80001357; PMID:111060

A:Accession: A90752

A:Molecule type: protein

A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-

R:Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A:Reference number: A93132; MUID:80114419; PMID:118920

A:Accession: A93132

A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOR>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90253; MUID:7203500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A:Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; MUID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds

C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM>

F:133-202/Domain: immunoglobulin homology <IM>

F:239-306/Domain: immunoglobulin homology <IM>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 52.2%; Score 1604; DB 1; Length 326;

Best Local Similarity 91.2%; Pred. No. 3.7e-83;

Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

RESULT 5

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A90333; A90249; A02150

R:Ellison, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

F:318/Binding site: carbohydrate (Aam) (covalent) #status predicted

Query Match 47.7%; Score 1466; DB 2; Length 470;

Best Local Similarity 61.5%; Pred. No. 3.3e-75;

Matches 280; Conservative 60; Mismatches 105; Indels 10; Gaps 6;

```
QY 1 EVTLVESGDFVKGKGLKVCASGAFSHYAMSWRQTPAKRLKLEWVAAYISGGSGSTYY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 QVLRRESGSLVRSQTLSTLCVSGFSLSYALTWRQAGKALEWVGITSGGT-TYY 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 SDVKGFTISRDNKAKTLYLQMSLSRSEDSAMVFCRVLKGT- -YFDSWGGGTTLV 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 79 NPALKSLSTIKENSKSQVLSVSVTPEDATATYCARSTYGEVGDGALMDAMQGLVLT 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 VSSASTGSPVFLPAPSCKSTSGTALGCLVKDYFPEPVTVMNSGALTSGVHTPAVL 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 VSSASTAPKVPPLSSCCGKSSSTVTLGCLVSSYMEPEPVTVMNSGALTSGVHTPAVL 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 QSSGLVLSSTVTPSSSLGTQTYICNVNHPKSTKDKKVEPKSCDKHTCPCPAPEL 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 QSSGLVLSSTVTPSSSLGTQTYICNVNHPKSTKDKKVEPKSCDKHTCPCPAPEL 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 LGSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 PGSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 315
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 297 QYNSTRVAVSLTVLHODMLNGEKYKCKVSNKALPAPIETKISAKQPREPQVYTLPPS 356
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 QFNSTRVAVSALRLOHODMTGCKEFCCKVHNEGIPAPIETVTSRTKPAEPQVYVLA 375
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 357 RDELTKVQSLTCLVKGFYPSDIAVEMESNQGP-ENNYKTPPVLDSDGSFFLYSKLT 414
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 376 QBELSKSTVSLTCLVTSFYFDYLAIVEMQNGPSESKGTTPQLDADSYFLSKLRV 435
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 DKSRMQGNVSCSVMEHALHNHYTKSLSPGK 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 436 DRMSMGQDGYTCVVMHEALHNHYTKSLSPGK 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 8

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37483

R/Duncan, F.F.D.

submitted to the EMBL Data Library, February 1993

A/Reference number: S37483

A/Accession: S37483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-469 <DUC>

A/Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 46.6%; Score 1430.5; DB 2; Length 469;

Best Local Similarity 58.8%; Pred. No. 3.2e-73;

Matches 266; Conservative 71; Mismatches 110; Indels 5; Gaps 4;

```
QY 1 EVTLVESGDFVKGKGLKVCASGAFSHYAMSWRQTPAKRLKLEWVAAYISGGSGSTYY 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 QVLRRESGSLVRSQTLSTLCVSGFSLSYALTWRQAGKALEWVGITSGGT-TYY 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 SDVKGFTISRDNKAKTLYLQMSLSRSEDSAMVFCRVLKGT- -YFDSWGGGTTLV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 NEFPKGAITLVDTSSSTAYMQLSLTSEDTAYFCRAMGATATLIDYGGGTTLVSS 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 ASIKGSPVFLPAPSCKSTSGTALGCLVKDYFPEPVTVMNSGALTSGVHTPAVL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 AKTAPASVFLPAPVCGDTTSSVTLGCLVKGYPPEPVTLMNSGSLSSGVHTPAVL 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 180 GLYSLSVTVTPSSSLGTQTYICNVNHPKSTKDKKVEPKSCDKHTCP-CPAPEL 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 -LTVLSSVTVTPSSSLGTQTYICNVNHPKSTKDKKVEPKSCDKHTCP-CPAPEL 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 238 GSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 GSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 YNSTRVAVSLTVLHODMLNGEKYKCKVSNKALPAPIETKISAKQPREPQVYTLPPS 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 YNSTRVAVSALRLOHODMTGCKEFCCKVHNEGIPAPIETVTSRTKPAEPQVYVLA 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 DELTKVQSLTCLVKGFYPSDIAVEMESNQGPENNYKTPPVLDSDGSFFLYSKLT 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 EELTKVQSLTCLVKGFYPSDIAVEMESNQGPENNYKTPPVLDSDGSFFLYSKLT 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 RMOGNVSCSVMEHALHNHYTKSLSPGK 449
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 NMVERNSVSCSVMEHALHNHYTKSLSPGK 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 9

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C/Accession: S69339; S72664

R/Khamlich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A/Reference number: S69339; NUID:95262687; PMID:7744049

A/Accession: S69339

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-374 <KHA>

A/Cross-references: EMBL:X81695

R/Khamlich, A.A.

submitted to the EMBL Data Library, September 1994

A/Reference number: S72664

A/Accession: S72664

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-140, C, 142-374 <KH2>

C/Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 46.3%; Score 1423; DB 2; Length 374;

Best Local Similarity 61.9%; Pred. No. 6.4e-73;

Matches 281; Conservative 23; Mismatches 46; Indels 104; Gaps 4;

```
QY 1 EVTLVESGDFVKGKGLKVCASGAFSH- -YAMSWRQTPAKRLKLEWVAAYISGGSGT 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 20 QVLRRESGSLVRSQTLSTLCVSGFSLSYALTWRQAGKALEWVGITSGGT-TYY 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 59 YNSDVKGFTISRDNKAKTLYLQMSLSRSEDSAMVFCRVLKGT- -YFDSWGGGTTLV 115
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 79 RYSPSLRTRTLTKDYSKQVLTMTNVPADATATYCGSVGEGYQGRFHSWGQTTLV 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 TVSSASTGSPVFLPAPSCKSTSGTALGCLVKDYFPEPVTVMNSGALTSGVHTPAVL 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 139 TVSS- - - - - - - - - - - - - - - - - - - - - - - - - - - - 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 176 LQSSGLVLSSTVTPSSSLGTQTYICNVNHPKSTKDKKVEPKSCDKHTCPCPAPE 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 160
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 236 LIGSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 161 LIGSPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMYVDGEVHNAAKTKEP 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 296 EQNSTYRVAVSLTVLHODMLNGEKYKCKVSNKALPAPIETKISAKQPREPQVYTLPP 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 221 EQNSTYRVAVSLTVLHODMLNGEKYKCKVSNKALPAPIETKISAKQPREPQVYTLPP 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


A:Molecule type: mRNA
 A:Residues: 1-474 <F5>
 A:Cross-references: UNIPROT:P01866; EMBL:X67210; NID:G54826; PIDD:CAA7649.1; PID:G54827
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Otsuka, M.; Honjo, T.
 Nature 283, 786-789, 1990
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A:Note: the sequence was determined from the germline gene
 R:Ucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
 A:Reference number: A26235; MUID:80081501; PMID:117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU1>
 A:Note: Lys-474 is probably removed posttranslationally
 R:Ucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
 A:Reference number: A26232; MUID:80081502; PMID:117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU2>
 R:Ollio, R.; Rougion, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
 A:Reference number: A26233; MUID:82173203; PMID:6803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-300, 'R', 302-331, 'A', 333-437, 'D', 440-474
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.
 C:Genetics:
 A:Introns: 138/1, 236/1, 258/1, 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Distal: interchain (to light chain) #status predicted
 F:164-220, 288-348, 394-452/Distal: interchain (to heavy chain) #status predicted
 F:247, 250, 253, 255/Distal: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.4%; Score 1365; DB 1; Length 474;
 Best Local Similarity 55.8%; Pred. No. 1,66-69;
 Matches 256; Conservative 72; Mismatches 117; Indels 14; Gaps 4;
 1 EYTLVSGDFFVKGSLKVCASGAFSHVAMSVROTAPKRLVAVYISGGSGTYY 60
 20 EYTLVSGDFFVKGSLKVCASGAFSHVAMSVROTAPKRLVAVYISGGSGTYY 79
 61 SDSVGRFTISRDNAKNTLYLQKRSLSRSDSAMYFCTRYKLTGY--YFDSMGQTTLY 117
 80 NEFKKATLTVDKSSSTVYLHLSLTSDSAYFACGPRQVGLRFGYWGQGLTVA 135

Query Match 43.7%; Score 1343.5; DB 2; Length 475;
 Best Local Similarity 55.4%; Pred. No. 2,56-68;
 Matches 253; Conservative 75; Mismatches 120; Indels 9; Gaps 4;
 1 EYTLVSGDFFVKGSLKVCASGAFSHVAMSVROTAPKRLVAVYISGGSGTYY 60
 20 QVQLQSGELARPGASVTLKSCASGYTLTISYGVSWKORTGQGLDWIGETIPYSGNSYP 79
 61 SDSVGRFTISRDNAKNTLYLQKRSLSRSDSAMYFCTRYKLTGY--YFDSMGQTTLY 119
 80 NEFKKATLTVDKSSSTVYLHLSLTSDSAYFACGPRQVGLRFGYWGQGLTVA 139
 120 ASKSGSVPLAPSSKSTGATLALCLVWDYPEPEVTYSWNSGALTSGLVPAVLAQSS 179
 140 AKTTPSVPLAPGCDITGSSVTLGLVKGYPESVYTYWNSGSLSSVHTPALLO-S 198
 180 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTRVKKVPEKSCDKT-RTCP-----CP 232
 199 GLYTMSSVTVTPSSSLGTQTYICNVNHPKSNTRVKKVPEKSCDKT-RTCP-----CP 258
 233 APELLGSPVPLAPGCDITGSSVTLGLVKGYPESVYTYWNSGSLSSVHTPALLO-S 252
 259 APTLGGSPVPLAPGCDITGSSVTLGLVKGYPESVYTYWNSGSLSSVHTPALLO-S 318
 293 PREQNSSTYRVSVTVLHODVNLGKYEYKCKVSNLAPAPIKRTISKAKGQPREPOVY 352

Db 319 THREDYNSITRVVSLPIQHDMWSGKEFKCVNNKDLPAPIERTISIKIGIVRAPQVYI 378
QY 353 LPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGQPENNYKTTTPVLDGSEFLYSKL 412
Db 379 LSPPEQLSRKDVSLTCLVGFSPEDISVEMTNSGTEENYKDTAPVLDGSEFLYSKL 438
QY 413 TVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 449
Db 439 NMKTSKWEKTDSPSCVVRHGLKNYYLKTISRSPGK 475

RESULT 14

147159
Ig gamma 2a chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_rev1stion 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47159
R/Kaczkovich, I., Sun, J., Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A/Reference number: I47158, M0ID:95015845, PMID:7930579
A/Accession: I47159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-328 <FAC>
A/Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C/Genetics:
A/Gene: IGG2a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
Fj133-202/Domain: immunoglobulin homology <ITM>

Query Match 41.1%; Score 1263; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 5.3e-64;

Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;

QY 120 ASTKGSVPPLAASSKSTSGCTALGLYKDYPPPEYTSWNSGALTSVHTPPAVLQSS 179
Db 1 APKTAASVYPLAPCSRDTSQPNVALGLASSYPPPEYTVWNSGALSSGVHTPPSVLQPS 60
QY 180 GLYSLSVTVPPSSISGTOTYICNVNHNKPESTKVDKKVPEKSCDKHTGCPAPAPLGG 239
Db 61 GLYSLSVTVPPSSISSTSYTCNVNHNKPESTKVDKKVPEKSCDKHTGCPAPAPLGG 116
QY 240 PSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFMYVDGVEVHNAKTKRREQYV 299
Db 117 PSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFMYVDGVEVHNAKTKRREQYV 176
QY 300 STYRVVSVLTTLHQMVLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 359
Db 177 STYRVVSVLTTLHQMVLNGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSRDE 236
QY 360 LTNGOYSLTCLVGFYPSDIAVWESNGQ--PENNYKTTTPVLDSDGSEFLYSKLTVDSK 417
Db 237 LSRSKVSLTCLVGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSEFLYSKLTVDSK 296
QY 418 RMQGNVFCSCVMHEALHNHYTKSLSLSPGK 449
Db 297 SMQGGGIFQCAVHHEALHNHYTKSLSLSPGK 328

RESULT 15

531866

Ig gamma-1 chain C region - synthetic

C/Species: synthetic

A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C/Date: 06-Jan-1995 #sequence_rev1stion 17-Mar-1997 #text_change 19-May-2000

C/Accession: S31866

R/Filpula, D.

submitted to the EMBL Data Library, February 1993

A/Description: Screening method for protein-protein interactions of cloned gene products.

A/Reference number: S31866

A/Accession: S31866

A/Molecule type: mRNA

A/Residues: 1-255 <FIL>
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C/Keywords: immunoglobulin
Fj1-22/Region: Escherichia coli outer membrane protein A precursor
Fj23-255/Region: human Ig gamma-1 chain C region

Query Match 41.0%; Score 1260; DB 4; Length 255;
Best Local Similarity 97.5%; Pred. No. 5.8e-64;
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 211 TVDKKVEPKSCDKHTGCPAPAPLGGSPVLPFPKPKDTLMTSRTEPVTCVVVDVSH 270
Db 17 TVAQADVSKSCDKHTGCPAPAPLGGSPVLPFPKPKDTLMTSRTEPVTCVVVDVSH 76
QY 271 EDPEVKFMYVDGVEVHNAKTKRREQYVSTYRVVSVLTTLHQMVLNGKEYCKVSNKAL 330
Db 77 EDPEVKFMYVDGVEVHNAKTKRREQYVSTYRVVSVLTTLHQMVLNGKEYCKVSNKAL 136
QY 331 PAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGQPE 390
Db 137 PAPIETKISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVGFYPSDIAVWESNGQPE 196
QY 391 NNYKTTTPVLDSDGSEFLYSKLTVDSKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 449
Db 197 NNYKTTTPVLDSDGSEFLYSKLTVDSKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 255

Search completed: December 23, 2004, 19:06:08

Job time : 33.449 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 18:31:20 ; Search time 161.904 Seconds
(without alignments)
2068.313 Million cell updates/sec

Title: US-10-089-500-57

Perfect score: 3071

Sequence: 1 EVTLVSSGSGDFVKGSLKV.....IVEFLNMTFCQSIISTLT 582

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: uniprot_02:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195.5	71.5	471	2	AAH24289
2	2184	71.1	470	2	Q6RJA4
3	2184	71.1	470	2	AAH18747
4	2184	71.1	478	2	Q6P181
5	2184	71.1	478	2	AAH41037
6	2166.5	70.5	475	2	Q6M206
7	2166.5	70.5	475	2	CAE45972
8	2166	70.5	472	2	BAC85232
9	2160	70.3	472	2	Q6N089
10	2157.5	70.3	472	2	CAE45781
11	2154.5	70.2	479	2	Q6GMW7
12	2154.5	70.2	479	2	AAH06402
13	2152.5	70.1	473	2	Q6MZV7
14	2152.5	70.1	473	2	CAE45920
15	2148	69.9	468	2	BAC85444
16	2146	69.9	480	2	Q6N094
17	2146	69.9	480	2	CAE45776
18	2145	69.8	466	2	Q6IN78
19	2140.5	69.7	544	2	Q6R195
20	2140.5	69.7	544	2	AAH19046
21	2126	69.2	466	2	Q6N096
22	2126	69.2	466	2	CAE45774
23	2124.5	69.2	473	2	Q6P055
24	2124.5	69.2	473	2	AAH65820
25	2124	69.2	470	2	Q7Z5M1
26	2123	69.1	478	2	BAC85385
27	2122	69.1	464	2	BAC85373
28	2120.5	69.0	471	2	BAC85388
29	2113	68.8	466	2	AAH64496
30	2111	68.7	482	2	Q7Z351
31	2105	68.5	470	2	BAC85172

32	2103	68.5	474	2	BAC85350
33	2095.5	68.2	479	2	AAH14667
34	2090	68.1	464	2	AAH19337
35	2088	68.0	468	2	BAC85175
36	2083	67.8	474	2	BAC85171
37	2080.5	67.7	481	2	Q6N097
38	2080.5	67.7	481	2	CAE45773
39	2066.5	67.3	469	2	Q7Z7P5
40	2057	67.0	470	2	AAH62336
41	2055	66.9	476	2	BAC05017
42	2054	66.9	472	2	BAC86225
43	2052.5	66.8	475	2	Q6N095
44	2052.5	66.8	475	2	CAE45775
45	2051	66.8	474	2	BAC05012

ALIGNMENTS

RESULT 1	
AAH24289	PRELIMINARY; PRT; 471 AA.
ID	AAH24289
AC	AAH24289;
DT	02-MAR-2004 (TrEMBLrel. 27, Created)
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxId=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=SpLeen;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner N., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA	DiGiuseppe L., Marubina K., Farmer A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.P., Prange C.,
RA	Brownstein M.J., Uddin T.B., Teshnyuk S., Carinini P., Mullaly S.J.,
RA	Raba S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gamaratre P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez M.A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Kryzhanovsk M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA	Jones S.J., Maxra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=SpLeen;
RA	Strausberg R.;
RA	Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC024289; AAH24289.1; -.
RN	Hypothetical protein.
SQ	SEQUENCE 471 AA; 51791 MW; 388F74CF588660E CRC64;
Query Match	71.5%; Score 2195.5; DB 2; Length 471;
Best Local Similarity	91.6%; Pred. No. 9.5e-133;
Matches	414; Conservative 16; Mismatches 19; Indels 3; Gaps 2
QY	1 EVTLVSSGSGDFVKGSLKVCASGPAFSAHVMVWRTQTPARLEWAVYISGGSGCTYY 60
DB	20 EVTLVSSGSGGLVKGSLKVCASGFTFSSYMNWVRQAPKGLWVSSSSSYIYY 79
QY	61 SDSVKGRFTTSRDNKNTLYLQWRSLSRSDSNAVYFCTR--VKGTGY-YFDSKQGGTTLTV 117

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Db      80 ADBVGRFTISRDNAMKNSLYLQWNSLRABEDTAVYCARDLRQRTSWYFDMRGSLTVV 139
QY      118 SASATGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNAGALTSGVHTFPAVLQ 177
Db      140 SASATGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNAGALTSGVHTFPAVLQ 199
QY      178 SSGLYSLSSVYVTPSSSLGTQTYICNVNHPKSTKYDKKVEPSCDKTHCPCPAPPELL 237
Db      200 SSGLYSLSSVYVTPSSSLGTQTYICNVNHPKSTKYDKKVEPSCDKTHCPCPAPPELL 259
QY      238 GGSVFLFPKPXDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKPREQ 297
Db      260 GGSVFLFPKPXDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKPREQ 319
QY      298 YNSTYRVSVLTLYLADMDLNGKEYKKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 357
Db      320 YNSTYRVSVLTLYLADMDLNGKEYKKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 379
QY      358 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 417
Db      380 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKS 439
QY      418 RMQGNVFCSCVMHEALHNNHYTKSLSPGK 449
Db      440 RMQGNVFCSCVMHEALHNNHYTKSLSPGK 471

RESULT 2
Q6PUA4 PRELIMINARY; PRT; 470 AA.
AC 06PUA4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.
TISSE=Primary B-Cells; PubMed=12477932;
MEDLINE=22388257;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchan J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC018747, AA018747.1, -.
DR InterPro, IPR003599, IG.
DR InterPro, IPR007110, IG_1like.
DR InterPro, IPR003597, IG_c1.

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DR InterPro, IPR003006, IG_MHC.
DR InterPro, IPR003596, IG_V.
DR Pfam, PF07654, C1-set; 3.
DR Pfam, PF00047, Ig; 4.
DR SMART, SM00409, Ig; 2.
DR SMART, SM00407, IGc1; 3.
DR SMART, SM00406, IGV; 1.
DR PROSITE, PS00835, IG_LIKE; 4.
DR PROSITE, PS00290, IG_MHC, UNKNOWN_2.
KW Hypothetical protein
SQ SEQUENCE 470 AA; 51715 MW; 784956A11FD7D9 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 470;
Best local Similarity 91.4%; Pred. No. 5, 2e-132;
Matches 412; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 1 EYTVESGGDFYKPGSLKVCASGPAFSHYAMSWROTPAKRLLEWVYISGSGSTTY 60
Db 20 EYTVESGGGLVQPGSLKVCASGFTFSSYWMWVRQAPGKLEWVANIQDGSSEKYY 79
QY 61 SDSVGRFTISRDNANKTLTYLQMRSLRSDSAMRYCTRYKLGTY--YFDSMGQGLTVYS 118
Db 80 VDSVGRFTISRDNAMKNSLYLQWNSLRABEDTAVYCARDGSSWYRDMFPMQGLTVYS 139
QY 119 SASATGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNAGALTSGVHTFPAVLQ 178
Db 140 SASATGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNAGALTSGVHTFPAVLQ 199
QY 179 SGLYSLSSVYVTPSSSLGTQTYICNVNHPKSTKYDKKVEPSCDKTHCPCPAPPELL 238
Db 200 SGLYSLSSVYVTPSSSLGTQTYICNVNHPKSTKYDKKVEPSCDKTHCPCPAPPELL 259
QY 239 GGSVFLFPKPXDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKPREQ 298
Db 260 GGSVFLFPKPXDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVNAATKPREQ 319
QY 299 NSTYRVSVLTLYLADMDLNGKEYKKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 358
Db 320 NSTYRVSVLTLYLADMDLNGKEYKKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 379
QY 359 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSR 418
Db 380 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSR 439
QY 419 MOGNVFCSCVMHEALHNNHYTKSLSPGK 449
Db 440 MOGNVFCSCVMHEALHNNHYTKSLSPGK 470

RESULT 3
AA018747 PRELIMINARY; PRT; 470 AA.
AC AA018747;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;

SEQUENCE FROM N.A.
TISSE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallie D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -
KM Hypothetical protein.
SO SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 470;
Best Local Similarity 91.4%; Pred. No. 5.2e-132;
Matches 412; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 1 EYLVESGDFVRPGSLKVCASGAFSHYMSWRTPAKLEWNAVYISSGSGTYY 60
DB 20 EVOLVESGGGLVPGSGLRSLSCVSGFTFSYMSWRQAGKLEWNAVNIKODGSEKYY 79
QY 61 SDYVKGFTISRDNKATLYLQNRSLRSEDSAMYFCTR--YFDSWGQSTTLVS 118
DB 80 VDSYVKGFTISRDNKATLYLQNRSLRSEDSAMYFCTR--YFDSWGQSTTLVS 139
QY 119 SASTKGSPVPLAPSSKSTSGCTALGCLVQDYPEPVTVSNAGALTSGVHTPEAVLQS 178
DB 140 SASTKGSPVPLAPSSKSTSGCTALGCLVQDYPEPVTVSNAGALTSGVHTPEAVLQS 199
QY 179 SGLYSLSSVTVPESSISGCTQYICNNVHKPSNTVDKVKPEKCDKTHTCPCAPBELLG 238
DB 200 SGLYSLSSVTVPESSISGCTQYICNNVHKPSNTVDKVKPEKCDKTHTCPCAPBELLG 259
QY 239 GPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVGVGHNAKTKPREBOY 298
DB 260 GPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVGVGHNAKTKPREBOY 319
QY 299 NSTYRVVSVTLVHLDWLNKGEYKCVSNKALPAPIEKTISKAKQPREPOVYTLPSRD 358
DB 320 NSTYRVVSVTLVHLDWLNKGEYKCVSNKALPAPIEKTISKAKQPREPOVYTLPSRD 379
QY 359 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSR 418
DB 380 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSR 439
QY 419 WQGNVSPCSYMHAEALHNHYTKSLSPGK 449
DB 440 WQGNVSPCSYMHAEALHNHYTKSLSPGK 470

RESULT 4
Q6P181 PRELIMINARY; PRT; 478 AA.
AC Q6P181;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
TI TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smallie D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-CL.
DR InterPro; IPR003506; IG_MHC.
DR InterPro; IPR003596; IG_Y.
DR Pfam; PF07654; Cl-sec; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SO SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 71.1%; Score 2184; DB 2; Length 478;
Best Local Similarity 90.0%; Pred. No. 5.3e-132;
Matches 413; Conservative 13; Mismatches 23; Indels 10; Gaps 2;

QY 1 EYLVESGDFVRPGSLKVCASGAFSHYMSWRTPAKLEWNAVYISSGSGTYY 60
DB 20 EVOLVESGGGLVPGSGLRSLSCVSGFTFSYMSWRQAGKLEWNAVNIKODGSEKYY 79
QY 61 SDYVKGFTISRDNKATLYLQNRSLRSEDSAMYFCTR-----VKLGYTF--DSWG 110
DB 80 VDSYVKGFTISRDNKATLYLQNRSLRSEDSAMYFCTR-----VKLGYTF--DSWG 139
QY 111 OGTTLVSSASTKGSPVPLAPSSKSTSGCTALGCLVQDYPEPVTVSNAGALTSGVH 170
DB 140 KGTTLVSSASTKGSPVPLAPSSKSTSGCTALGCLVQDYPEPVTVSNAGALTSGVH 199
QY 171 TFPVAVLQSSGLYSLSSVTVPESSISGCTQYICNNVHKPSNTVDKVKPEKCDKTHTCPP 230
DB 200 TFPVAVLQSSGLYSLSSVTVPESSISGCTQYICNNVHKPSNTVDKVKPEKCDKTHTCPP 259
QY 231 CPAPELLGSPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVGVGHNAK 290
DB 260 CPAPELLGSPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNNYVGVGHNAK 319
QY 291 TKPREBOYNTYRVVSVTLVHLDWLNKGEYKCVSNKALPAPIEKTISKAKQPREPOV 350
DB 320 TKPREBOYNTYRVVSVTLVHLDWLNKGEYKCVSNKALPAPIEKTISKAKQPREPOV 379
QY 351 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLY 410
DB 380 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLY 439

QY 411 KLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 449
DB 440 KLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 478

RESULT 5
AAH41037 PRELIMINARY; PRT; 478 AA.

ID AAH41037
AC AAH41037;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cell; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cell;
RA Strausberg R.;
RU Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
KW Hypothetical protein.

QY SEQUENCE 478 AA; 52666 MW; 178BD38D917970D6 CRC64;
Query Match 71.1%; Score 2184; DB 2; Length 478;
Best Local Similarity 90.0%; Pred. No. 5.3e-132;
Matches 413; Conservative 13; Mismatches 23; Indels 10; Gaps 2;

QY 1 EYTLVSGGDFVFKPGSLKVCASGFAFSGHYAMSVROTPAKRLBMAVYISSGSGGTY 60
DB 20 EYGLVSGGGLVQPGSLRLSCAASGFTFSYMSVVRAPKGLBMAVNIKDGSEKTY 79
QY 61 SDSVKGKFTISRDNKNTLYLQMSLRSEDSAMFYCTRYLGTYYF--DSMG 110
DB 80 VDSVKGKFTISRDNKNTLYLQMSLRSEDSAMFYCTRYLGTYYF--DSMG 139
QY 111 OGTLTVSSASSTGSPVFPPLAPSSKSTSGGTALGCLVQDFPEPVTVMNSGALTSGVHTP 170
DB 140 KGTIVVSSASTGSPVFPPLAPSSKSTSGGTALGCLVQDFPEPVTVMNSGALTSGVHTP 199
QY 171 TFPVAVQSSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKVPEKSCDKHTTCCP 230
DB 200 TFPVAVQSSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKVPEKSCDKHTTCCP 259
QY 231 CPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAAK 290

DB 260 CPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAAK 319
QY 291 TKPREQYNSTYRVYSLTVLHODMVLNGEKYCKYCNKALPAPIETKISKAGQPREPOV 350
DB 320 TKPREQYNSTYRVYSLTVLHODMVLNGEKYCKYCNKALPAPIETKISKAGQPREPOV 379
QY 351 YTLPPSRDELITNQNVSITGLVGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYS 410
DB 380 YTLPPSRDELITNQNVSITGLVGFYPSDIAVEMESNGQPENNYKTPPVLDSDGSFFLYS 439
QY 411 KLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 449
DB 440 KLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 478

RESULT 6
Q6MZ06 PRELIMINARY; PRT; 475 AA.

ID Q6MZ06
AC Q6MZ06;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G1190.
GN Name=DKFZp686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG THE GERMAN HUMAN CDNA CONSORTIUM;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RU Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003597; Ig CL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IgC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
QY SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 70.5%; Score 2166.5; DB 2; Length 475;
Best Local Similarity 89.0%; Pred. No. 7e-131;
Matches 406; Conservative 18; Mismatches 25; Indels 7; Gaps 1;

QY 1 EYTLVSGGDFVFKPGSLKVCASGFAFSGHYAMSVROTPAKRLBMAVYISSGSGGTY 60
DB 20 EYGLVSGGGLVQPGSLRLSCAASGFTFSYMSVVRAPKGLBMAVNIKDGSEKTY 79
QY 61 SDSVKGKFTISRDNKNTLYLQMSLRSEDSAMFYCTRYLGTYYF--YFDSMGQGT 113
DB 80 ADSVKGKFTISRDNKNTLYLQMSLRSEDSAMFYCTRYLGTYYF--YFDSMGQGT 139
QY 114 TLTVSSASSTGSPVFPPLAPSSKSTSGGTALGCLVQDFPEPVTVMNSGALTSGVHTP 173
DB 140 LVTVSSASSTGSPVFPPLAPSSKSTSGGTALGCLVQDFPEPVTVMNSGALTSGVHTP 199
QY 174 AVTQSSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKVPEKSCDKHTTCCP 233
DB 200 AVTQSSGLYSLSSVTVTPSSSLGTQTYICNVNKKPSNTKVDKKVPEKSCDKHTTCCP 259
QY 234 PELGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYVDGVEVHNAAK 293

Db 260 PELGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKP 319

Qy 294 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 353

Db 320 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 379

Qy 354 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 413

Db 380 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 439

Qy 414 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 440 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 7

CAB45972 PRELIMINARY; PRT; 475 AA.

AC CAB45972; (Tremblrel. 27, Created)

DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)

DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686g1190.

GN DKFZp686g1190.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;

RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Oesinger A., Fobo G.,

RA Han M., Wiemann S.,

RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX40947; CAB45972.1; -.

KW Hypothetical protein.

SQ SEQUENCE 475 AA; 52043 MW; B7EA255A26F4B8E CRC64;

Query Match 70.5%; Score 2166.5; DB 2; Length 475;

Best Local Similarity 89.0%; Pred. No. 7e-131;

Matches 406; Conservative 18; Mismatches 25; Indels 7; Gaps 1;

Qy 1 EYTLVESGDPFVKRGSLKYSKAASGAFSHYMSWTRQPAKRLKLVAVYISGSGSTYY 60

Db 20 EYTLVESGDPFVKRGSLKYSKAASGAFSHYMSWTRQPAKRLKLVAVYISGSGSTYY 79

Qy 61 SDSVKGFTISRDNKNTLYLQKRSLSRSDSAMYFCTRYLGTYY-----YFDSMGQGT 113

Db 80 ADSVKGFTISRDNKNTLYLQKRSLSRSDSAMYFCTRYLGTYY-----YFDSMGQGT 139

Qy 114 TLTVSSASTGSPVFLPABSSKTSISGTAALGCLVKDYFPEPVTVSNVNSGALTSGVHTFP 173

Db 140 LVSVAASATGSPVFLPABSSKTSISGTAALGCLVKDYFPEPVTVSNVNSGALTSGVHTFP 199

Qy 174 AVTQSSGLYSLSVAVTPSSSLGTQTYICNVNHPSTKVDKKEPKSCDKTHPCPCPA 233

Db 200 AVTQSSGLYSLSVAVTPSSSLGTQTYICNVNHPSTKVDKKEPKSCDKTHPCPCPA 259

Qy 234 PELGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKP 293

Db 260 PELGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKP 319

Qy 294 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 353

Db 320 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 379

Qy 354 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 413

Db 380 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 439

Qy 414 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 440 VDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 8

BAC85232 PRELIMINARY; PRT; 472 AA.

AC BAC85232; (Tremblrel. 27, Created)

DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)

DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)

DE CDNA FLJ26265 f18, clone DMC0516, highly similar to Ig gamma-1 chain C region.

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Dermoid tumor;

RA Oca T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,

RA Hata H., Nakagawa K., Mizuno S., Morigawa M., Kawamura M.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,

RA Kawakami B., Nagai K., Isegai T., Sugano S.,

RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK129776; BAC85232.1; -.

SQ SEQUENCE 472 AA; 51212 MW; 01BF215F99809164 CRC64;

Query Match 70.5%; Score 2166; DB 2; Length 472;

Best Local Similarity 89.2%; Pred. No. 7.5e-131;

Matches 406; Conservative 18; Mismatches 23; Indels 8; Gaps 2;

Qy 1 EYTLVESGDPFVKRGSLKYSKAASGAFSHYMSWTRQPAKRLKLVAVYISGSGSTYY 60

Db 20 EYTLVESGDPFVKRGSLKYSKAASGAFSHYMSWTRQPAKRLKLVAVYISGSGSTYY 79

Qy 61 SDSVKGFTISRDNKNTLYLQKRSLSRSDSAMYFCTRYLGTYY-----YFDSMGQGT 114

Db 80 ADSVKGFTISRDNKNTLYLQKRSLSRSDSAMYFCTRYLGTYY-----YFDSMGQGT 137

Qy 115 LTVSSASTGSPVFLPABSSKTSISGTAALGCLVKDYFPEPVTVSNVNSGALTSGVHTFP 174

Db 138 LTVSSASTGSPVFLPABSSKTSISGTAALGCLVKDYFPEPVTVSNVNSGALTSGVHTFP 197

Qy 175 VLOSSGLYSLSVAVTPSSSLGTQTYICNVNHPSTKVDKKEPKSCDKTHPCPCPA 234

Db 198 VLOSSGLYSLSVAVTPSSSLGTQTYICNVNHPSTKVDKKEPKSCDKTHPCPCPA 257

Qy 235 ELGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKP 294

Db 258 ELGGSPVFLPPPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKP 317

Qy 295 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 354

Db 318 REEQYNSTRVSVLTVLHODMLNGKEYKCKVSKKALPAPIEKTISAKGQPREPOVYTL 377

Qy 355 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 414

Db 378 PPSRDELTKQVSLTCLVKGFPSPDIAVEMESNQPENNYKTPPVLDSDGSFPLYSKLT 437

Qy 415 DKSRRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

Db 438 DKSRRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 472

RESULT 9

Q6N089 PRELIMINARY; PRT; 472 AA.

AC Q6N089; (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686p15220.

GN Name=DKFZp686p15220;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Mambuti R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_Like; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 70.3%; Score 2160; DB 2; Length 472;

Best Local Similarity 89.9%; Pred. No. 1.8e-130;

Matches 408; Conservative 16; Mismatches 24; Indels 6; Gaps 3;

QY 1 EYLVESGGDFYKPGSLKVCASGFAFSHYAMSVNQTPAKRLBMAVYISGSGSTY 60
DB 20 EYLVESGGGLVQPGSLRLSCASGFTDDYAMHVRQAPGKLEWVSGISMSGSIX 79
QY 61 SDSVKGRTISRDNAKNTLYLQMSLRSEDSAMYFCTRYKLT--YF--DSMGQITL 115
DB 80 ADSVKGRTISRDNKNSLYLQMSLRSEDSAMYFCTRYKLT--YF--DSMGQITL 138
QY 116 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 175
DB 139 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 198
QY 176 LOSGGLYSLSSVYTVSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHCPCPAPE 235
DB 199 LOSGGLYSLSSVYTVSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHCPCPAPE 258
QY 236 LLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTKPRE 295
DB 259 LLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTKPRE 318
QY 296 EGYNSTYRVSVLYTLVHQMNLNGEKYCKVSNKALPAPIEKTISAKQGPREFQVYTLTP 355
DB 319 EGYNSTYRVSVLYTLVHQMNLNGEKYCKVSNKALPAPIEKTISAKQGPREFQVYTLTP 378
QY 356 SRDELTKNOVSLTCLVKGFPSPDIAYEWESNQGPNNTKTPPVLDSDGSFYLKSLTYD 415
DB 379 SRDELTKNOVSLTCLVKGFPSPDIAYEWESNQGPNNTKTPPVLDSDGSFYLKSLTYD 438
QY 416 KSRWQGNVFCSCVNHAEALHNHYTKSLISLSPGK 449
DB 439 KSRWQGNVFCSCVNHAEALHNHYTKSLISLSPGK 472

RESULT 10

CAE45781 PRELIMINARY; PRT; 472 AA.
AC CAE45781;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686P15220.
GN DKFP686P15220.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Mambuti R., Heubner D., Mewes H.W., Weill B., Amid C., Osanger A.,
RA Fobio G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 70.3%; Score 2160; DB 2; Length 472;

Best Local Similarity 89.9%; Pred. No. 1.8e-130;

Matches 408; Conservative 16; Mismatches 24; Indels 6; Gaps 3;

QY 1 EYLVESGGDFYKPGSLKVCASGFAFSHYAMSVNQTPAKRLBMAVYISGSGSTY 60
DB 20 EYLVESGGGLVQPGSLRLSCASGFTDDYAMHVRQAPGKLEWVSGISMSGSIX 79
QY 61 SDSVKGRTISRDNAKNTLYLQMSLRSEDSAMYFCTRYKLT--YF--DSMGQITL 115
DB 80 ADSVKGRTISRDNKNSLYLQMSLRSEDSAMYFCTRYKLT--YF--DSMGQITL 138
QY 116 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 175
DB 139 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFP 198
QY 176 LOSGGLYSLSSVYTVSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHCPCPAPE 235
DB 199 LOSGGLYSLSSVYTVSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKHTHCPCPAPE 258
QY 236 LLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTKPRE 295
DB 259 LLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVNAKTKPRE 318
QY 296 EGYNSTYRVSVLYTLVHQMNLNGEKYCKVSNKALPAPIEKTISAKQGPREFQVYTLTP 355
DB 319 EGYNSTYRVSVLYTLVHQMNLNGEKYCKVSNKALPAPIEKTISAKQGPREFQVYTLTP 378
QY 356 SRDELTKNOVSLTCLVKGFPSPDIAYEWESNQGPNNTKTPPVLDSDGSFYLKSLTYD 415
DB 379 SRDELTKNOVSLTCLVKGFPSPDIAYEWESNQGPNNTKTPPVLDSDGSFYLKSLTYD 438
QY 416 KSRWQGNVFCSCVNHAEALHNHYTKSLISLSPGK 449
DB 439 KSRWQGNVFCSCVNHAEALHNHYTKSLISLSPGK 472

RESULT 11

Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA MEDLINE=2388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -
DR InterPro; IPR003599; IG-
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sect; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PSS0290; IG MHC; UNKNOWN_2.
KM Hypothetical protein.
SO SEQUENCE 475 AA; 51987 MW; 2A1F55D736860F8 CRC64;

Query Match 70.3%; Score 2157.5; DB 2; Length 475;
Best Local Similarity 89.5%; Pred. No. 2.6e-130;
Matches 408; Conservative 15; Mismatches 26; Indels 7; Gaps 2;

QY 1 EYTVLSEGGDFVPRGSLKVCSCAAGPASHYAMSWROTPARKLEWNAVYISGSGSTGY 60
DB 20 EVGLVBSGGGLVOPGSLRLSCVSAFTLSRHAHMHVROAPGKGLVYSGISNSNSTY 79
QY 61 SDSVKGFRFTSRDNKATLYLQMSLRSEDSAMVFCRVR-----LGTYY-PDSWGQGT 113
DB 80 ADSVKGFRFTSRDNKATLYLQMSLRSEDSAMVFCRVR-----LGTYY-PDSWGQGT 139
QY 114 TLTVSSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNWNGALTSVHTFP 173
DB 140 TVIVSSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNWNGALTSVHTFP 199
QY 174 AVIQQSGLVSLSSVTVVPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTPCPCA 233
DB 200 AVIQQSGLVSLSSVTVVPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTPCPCA 259
QY 234 PELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAATKP 293
DB 260 PELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNAATKP 319
QY 294 REEQYNSTYRVSVTLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQYTL 353
DB 320 REEQYNSTYRVSVTLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQYTL 379
QY 354 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKT 413
DB 380 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKT 439
QY 414 VDSKRWQOGNVFSCSVNHEALHNHYTOKSLSPGK 449
DB 440 VDSKRWQOGNVFSCSVNHEALHNHYTOKSLSPGK 475

RESULT 12

AAH06402
ID AAH06402 PRELIMINARY; PRT; 479 AA.
AC AAH06402;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Vallat D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.,
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC06402; AAH06402.1; -
KM Hypothetical protein.
SO SEQUENCE 479 AA; 52281 MW; D74E0C9802A29788 CRC64;

Query Match 70.2%; Score 2154.5; DB 2; Length 479;
Best Local Similarity 88.7%; Pred. No. 4.2e-130;
Matches 408; Conservative 15; Mismatches 26; Indels 11; Gaps 2;

QY 1 EYTVLSEGGDFVPRGSLKVCSCAAGPASHYAMSWROTPARKLEWNAVYISGSGSTGY 60
DB 20 EVGLVBSGGGLVOPGSLRLSCVSAFTLSRHAHMHVROAPGKGLVYSGISNSNSTY 79
QY 61 SDSVKGFRFTSRDNKATLYLQMSLRSEDSAMVFCRVR-----LGTYY-PDSWGQGT 109
DB 80 ADSVKGFRFTSRDNKATLYLQMSLRSEDSAMVFCRVR-----LGTYY-PDSWGQGT 139
QY 110 TLTVSSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNWNGALTSVHTFP 169
DB 140 TVIVSSASTKGPVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSNWNGALTSVHTFP 199
QY 170 HTEPAVLOSGLVSLSSVTVVPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTPC 229
DB 200 HTEPAVLOSGLVSLSSVTVVPSSSLGTQTYICNVNHPKSTKVDKVEPKSCDKHTPC 259
QY 230 PCPAPILLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNA 289
DB 260 PCPAPILLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFMWYVDGVEVNA 319
QY 290 KTKPREEQYNSTYRVSVTLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQ 349
DB 320 KTKPREEQYNSTYRVSVTLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQ 379
QY 350 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLY 409

DB 380 VTTLPSSRDELTKNQSLTCLVKGFPSPDIAVWESNQGPPNNYKTTTPVLDSDGSFFLYSKLTVD 439
QY 410 SKLTUDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 449
DB 440 SKLTUDKSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 479

RESULT 13

Q6MZV7 PRELIMINARY, PRT, 473 AA.
ID Q6MZV7
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_Y.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFCA47 CRC64;

Query Match 70.1%; Score 2152.5; DB 2; Length 473;

Best Local Similarity 88.3%; Pred. No. 5.5e-130; Indels 5; Gaps 1;
Matches 401; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

QY 1 ETVLVESGGDFVYKPGGSLKVSCAASGFAFSHYAMSVWROTPAKRLBMAVYISGSGSTYY 60
DB 20 EIQVLVESGGGLVQPGGSLRLSCAASGFTSSPEMNMVWQAPGKGLMISYITRSGNTVYY 79
QY 61 SDSVGRFTISRDNANKTLYLQMRSLRSDSAMYCTRYKLGTF----YFPDWSGCGTTL 115
DB 80 ADSLQGRFTISRDNANSLYLQMNLSLRADDTAVYVCARQNEHTSPWYPSFFDWMGCGILV 139
QY 116 TVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSVHFFPAV 175
DB 140 TVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSNMGSALTSVHFFPAV 199
QY 176 LOSGGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDHTHTCPCPAPE 235
DB 200 LOSGGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDHTHTCPCPAPE 259
QY 236 LIGGSPVFLPFPKPKDTLMIISRTPEVTCVVDVSHEDPEVKENMYVDGVEVNAKTKPRE 295
DB 260 LIGGSPVFLPFPKPKDTLMIISRTPEVTCVVDVSHEDPEVKENMYVDGVEVNAKTKPRE 319
QY 296 EGYNSTYRVAIVTLVHQMNLNGEKYKCKVSNKALPAPIEKTISKAKQPREPOVYTLTP 355
DB 320 EGYNSTYRVAIVTLVHQMNLNGEKYKCKVSNKALPAPIEKTISKAKQPREPOVYTLTP 379
QY 356 SRDELTKNQVSLTCLVKGFPSPDIAVWESNQGPPNNYKTTTPVLDSDGSFFLYSKLTVD 415

DB 380 SREEMTKNQVSLTCLVKGFPSPDIAVWESNQGPPNNYKTTTPVLDSDGSFFLYSKLTVD 439
QY 416 KSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 473

RESULT 14

CAB45920 PRELIMINARY, PRT, 473 AA.
ID CAB45920;
AC CAB45920;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAB4C0BFCA47 CRC64;

Query Match 70.1%; Score 2152.5; DB 2; Length 473;

Best Local Similarity 88.3%; Pred. No. 5.5e-130; Indels 5; Gaps 1;
Matches 401; Conservative 24; Mismatches 24; Indels 5; Gaps 1;

QY 1 ETVLVESGGDFVYKPGGSLKVSCAASGFAFSHYAMSVWROTPAKRLBMAVYISGSGSTYY 60
DB 20 EIQVLVESGGGLVQPGGSLRLSCAASGFTSSPEMNMVWQAPGKGLMISYITRSGNTVYY 79
QY 61 SDSVGRFTISRDNANKTLYLQMRSLRSDSAMYCTRYKLGTF----YFPDWSGCGTTL 115
DB 80 ADSLQGRFTISRDNANSLYLQMNLSLRADDTAVYVCARQNEHTSPWYPSFFDWMGCGILV 139
QY 116 TVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNMGSALTSVHFFPAV 175
DB 140 TVSSASTKPSVPLAPSSKSTSGGTAALGCLVKDYFLEPVTVSNMGSALTSVHFFPAV 199
QY 176 LOSGGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDHTHTCPCPAPE 235
DB 200 LOSGGLYSLSSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDHTHTCPCPAPE 259
QY 236 LIGGSPVFLPFPKPKDTLMIISRTPEVTCVVDVSHEDPEVKENMYVDGVEVNAKTKPRE 295
DB 260 LIGGSPVFLPFPKPKDTLMIISRTPEVTCVVDVSHEDPEVKENMYVDGVEVNAKTKPRE 319
QY 296 EGYNSTYRVAIVTLVHQMNLNGEKYKCKVSNKALPAPIEKTISKAKQPREPOVYTLTP 355
DB 320 EGYNSTYRVAIVTLVHQMNLNGEKYKCKVSNKALPAPIEKTISKAKQPREPOVYTLTP 379
QY 356 SRDELTKNQVSLTCLVKGFPSPDIAVWESNQGPPNNYKTTTPVLDSDGSFFLYSKLTVD 415
DB 380 SREEMTKNQVSLTCLVKGFPSPDIAVWESNQGPPNNYKTTTPVLDSDGSFFLYSKLTVD 439
QY 416 KSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 449
DB 440 KSRWQGNVFCSVNHEALHNHYTQKSLSLSPGK 473

RESULT 15

BAC85444 PRELIMINARY, PRT, 468 AA.
ID BAC85444;
AC BAC85444;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (Tremblurel. 27, last sequence update)
DE 02-MAR-2004 (Tremblurel. 27, last annotation update)
DE CDNA FLJ27334 f18, clone TMS09201, highly similar to Ig gamma-1 chain
DE C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Tymus;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hara H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130844; BAC5444.1; -
SQ SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;

Query Match 69.9%; Score 2148; DB 2; Length 468;
Best Local Similarity 89.7%; Pred. No. 1.1e-129;

Matches 400; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 4 LVEGCDPVRPGSLKVCASGPAFSTYMSWROTPAKRLWVAIYSSGSGTYSDS 63
DB 23 LVEGGGLVKEGSLRLSCSASGFTSDYMGWTRQAPGKLEWISYISDGLSQYAES 82
QY 64 VKGRFTSRDIAKATLYLQNRSLRSEDSAMFCTRVKLGTYFPDSWGQGTLLTVSSASTK 123
DB 83 VKGRFTSRDIAKATLYLQNRSLRSEDSAMFCTRVKLGTYFPDSWGQGTLLTVSSASTK 142
QY 124 GPSVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 183
DB 143 GPSVFPPLAPSSKSTSGGTALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS 202
QY 184 LSSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGSPVF 243
DB 203 LSSVVTVPSSSLGTQTYICNNHKPSNTKVDKVEPKSCDKTHTCPCPAPPELLGSPVF 262
QY 244 LFPKPKDITMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPREEQYNSTYR 303
DB 263 LFPKPKDITMISRTPEVTCVVDVSHEDPEVKFNMVYDGVENHNAKTKPREEQYNSTYR 322
QY 304 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 363
DB 323 VVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKN 382
QY 364 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQGN 423
DB 383 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRWQGN 442
QY 424 VFGSVVHREALHNYTQKSLSLSPGK 449
DB 443 VFGSVVHREALHNYTQKSLSLSPGK 468

Search completed: December 23, 2004, 19:04:41
Job time : 162.904 secs

